



PD 11-JUL-2002

Region	48. .63
FT	





ADX98269  
 ID ADX98269 standard; protein; 140 AA.  
 AC ADX98269;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Human anti-HGF antibody heavy chain variable region protein - SEQ 41.  
 XX  
 KM antibody; cytostatic; cancer; neoplasm; solid tumor;  
 KM hepatocyte growth factor; HGF; light chain variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005017107-A2.  
 XX  
 PD 24-FEB-2005.  
 XX  
 PF 16-JUL-2004; 2004WO-US018936.  
 XX  
 PR 18-JUL-2003; 2003US-0488681P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Burgess TL, Coxon A, Green LL, Zhang K;  
 DR WPI; 2005-182350/19.  
 XX  
 DR N-PSDB; ADX98246.  
 XX  
 PT New polypeptide comprising a complementarity determining region (CDR)  
 PT consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of  
 PT binding hepatocyte growth factor, useful in preparing a composition for  
 PT treating cancer.  
 XX  
 PS Claim 9; SEQ ID NO 41; 301pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide comprising at least  
 CC one complementarity-determining region (CDR) consisting of CDR1a, CDR2a  
 CC or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with  
 CC an antibody heavy or light chain, is capable of binding hepatocyte growth  
 CC factor (HGF). HGF, also known as scatter factor (SF), has been identified  
 CC as a potent mitogen for hepatocytes and also as a secretory protein of  
 CC fibroblasts and smooth muscles that acts to induce motility of epithelial  
 CC cells. The polypeptide demonstrates cytostatic activity and may be useful  
 CC in preparing a composition for treating cancer or a solid tumor. The  
 CC current sequence is that of the human anti-HGF antibody heavy chain  
 CC variable region protein - SEQ 41 of the invention.  
 XX  
 SQ Sequence 140 AA;  
 Query Match 83.8%; Score 514.5; DB 9; Length 140;  
 Best Local Similarity 84.5%; Pred. NO. 4.4e-36;  
 Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;  
 QY 2 ESGGGLVPSQTLTLCTVSGSGSIRSGGYVSWVROPKGLKLEWIGNIYHSGNTYVPSL 61  
 Db 25 ESGGGLVXPSQTLTLCTVSGSGSISGGYVSWVRQHPGKLEWIGNIYHSGNTYVPSL 84  
 QY 62 KSRITMSVDTSKNHFSLRLISVTADTAIVVYCARSS---DGYTLDNWGQGITLVTVSS 114  
 Db 85 KSRVTMSVDTSKNHFSLRLISVTADTAIVVYCARDPYGVGDFPWCQGITLVTVSS 140  
 RESULT 6  
 ADP22124  
 ID ADP22124 standard; protein; 128 AA.  
 AC ADP22124;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:30.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KM antibacterial; antiinflammatory; antipsoriatic; antirheumatic;  
 KM neuroprotective; immunomodulator; immunosuppressive; nephrotropic;  
 KM TNF induced apoptosis; neoplastic disease; breast cancer;  
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KM prostate cancer; immuno-mediated inflammatory disease;  
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KM restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KM septic shock; cachexia; anorexia; multiple sclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004050683-A2.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 PR 02-DEC-2002; 2002US-0430729P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 DR WPI; 2004-480601/45.  
 DR N-PSDB; ADP22123.  
 XX  
 PT New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 30; 213pp; English.  
 XX  
 CC The present invention describes a human monoclonal antibody (1) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFa in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNFa in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFa induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFa antagonist. The antibody (1) is useful in the preparation of  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 128 AA;

Query Match	83.2%	Score 511	DB 8	Length 128
Best Local Similarity	78.9%	Pred. No. 7.9e-36		
Matches	97	Conservative	7	Mismatches 9
			Indels	10
			Gaps	1
Qy	2	ESGGLVLPSPQTLSTLTCTVSGGSIISGGYVSWVRPQPKGLEWIGNITGNTTYNSL	61	
Db	6	ESGGLVLPSPQTLSTLTCTVSGGSIISGGYVSWVRPQPKGLEWIGNITGNTTYNSL	65	
Qy	62	KSRTMSVDTSKNHFSLRLTSTVADTAIVVYCARSDG-----YTLDMNGGLT	111	
Db	66	KSRTVISTDTSKNHFSLRLTSTVADTAIVVYCARSDGNYNMNDEYVDGLDVGQGTIVT	125	
Qy	112	VSS 114		
Db	126	VSS 128		
RESULT 7				
ADP22104				
ID	ADP22104	standard; protein; 128 AA.		
XX	ADP22104;			
XX	AC			
XX	ADP22104;			
XX	DT	09-SEP-2004 (first entry)		
XX	DE	Human anti-TNFa antibody heavy chain variable region SEQ ID NO:10.		
XX	XX	human; monoclonal antibody; tumor necrosis factor-alpha; TNFa;		
XX	KM	anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;		
XX	KM	antibacterial; antiinflammatory; antipsoriatic; antirheumatic;		
XX	KM	eating-disorder; immunomodulator; immunosuppressive; nephrotropic;		
XX	KM	neuroprotective; vasotropic; antiapoptotic; TNF antagonist;		
XX	KM	TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;		
XX	KM	bladder cancer; lung cancer; glioblastoma; stomach cancer;		
XX	KM	endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;		
XX	KM	prostate cancer; immuno-mediated inflammatory disease; psoriasis;		
XX	KM	rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;		
XX	KM	restenosis; autoimmune disease; Crohn's disease; graft-host reaction;		
XX	KM	septic shock; cachexia; anorexia; multiple sclerosis.		
XX	OS	Homo sapiens.		
XX	XX			
XX	PN	WO2004050683-A2.		
XX	PD	17-JUN-2004.		
XX	XX			
XX	PE	02-DEC-2003; 2003KO-US038281.		
XX	XX			
XX	PR	02-DEC-2002; 2002US-0430729P.		
XX	XX			
XX	PA	(ABGE-) ABGENIX INC.		
XX	PI	Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;		
XX	PI	Haak-Frendscho W, Kathanaaswami P, Pigott C, Liang ML, Lee R;		
XX	PI	Manchuluenho K, Fegjioni R, Senaldi G, Qiaojuan JS;		
XX	XX			
XX	DR	WPI; 2004-480601/45.		
XX	DR	N-PSDB; ADP22103.		
XX	XX			
XX	PT	New recombinant human monoclonal antibody that specifically binds to		
XX	PT	Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such		
XX	PT	as cancers, or immuno-mediated inflammatory diseases such as rheumatoid		
XX	PT	arthritis.		
XX	PS	Example 10; SEQ ID NO 10; 213pp; English.		
XX	XX			
XX	CC	The present invention describes a human monoclonal antibody (I) that		
XX	CC	specifically binds to tumor necrosis factor-alpha (TNFa) and comprises:		
XX	CC	(a) a heavy chain complementarity determining region 1 (CDR1) having the		
XX	CC	two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);		
XX	CC	and (b) a light chain CDR1 having the two fully defined 11 amino acid		
XX	CC	sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying		
XX	CC	(MI) the level of TNFa in a patient sample, comprising contacting with		

(1), and detecting the level of binding between the antibody and TNFa in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced apoptosis in an animal by selecting an animal in need of treatment for TNFa induced apoptosis by administering the human monoclonal antibody of (1). (1) has antitumor, antiarteriosclerotic, antiarthritic, antibacterial, antiinflammatory, antiproliferative, antihemetic, eating-disorders, immunomodulator, immunosuppressive, nephrotoxic, neuroprotective, vasotropic and antiapoptotic activities, and can be used as a TNFa antagonist. The antibody (1) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody heavy chain variable region, which is used in the exemplification of the present invention.

Seq Sequence 128 AA;

Query Match 83.2%; Score 511; DB 8; Length 128;  
Best Local Similarity 78.9%; Pred. No. 7.9e-36;  
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY 2 ESGGGLVKPSTSLTCTVSGSGIRSGGYWWRQPPGKLEIGNIYHSGNYNPSL 61  
|||  
DB 6 ESGGGLVPSSTSLTCTVSGSGISSGGYWWSWRQPPGKLEIGNIYHSGNYNPSL 65  
|||  
QY KSRITMSVDTSKNHPSRLTSLVTADPAVYVYCARSDG-----YTLDNMQGELVT 111  
|||  
DB 66 KSRITISVDTSKNQPSLKTSSVTADPAVYVYCARSDNQYMNDEVDYGLDVMQGELVT 125  
|||  
QY 112 VSS 114  
|||  
DB 126 VSS 128

RESULT 8  
ADP22096  
ID ADP22096 standard; protein; 128 AA.  
XX  
AC ADP22096;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:2.  
XX  
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;  
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;  
KW antibacterial; antiinflammatory; antiproliferative; antihemetic;  
KW eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;  
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
KW prostate cancer; immuno-mediated inflammatory disease;  
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
KW septic shock; cachexia; anorexia; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004050683-A2.  
XX  
PD 17-JUN-2004.  
XX  
PF 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.  
 XX (ABGE-) ABGENIX INC.  
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 XX Heak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 XX Manchulenchu K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX WPI; 2004-480601/45.  
 XX N-PSDB; ADP22095.  
 XX New recombinant human monoclonal antibody that specifically binds to  
 XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 XX arthritis.  
 XX Example 10; SEQ ID NO 2; 213pp; English.  
 XX The present invention describes a human monoclonal antibody (I) that  
 XX specifically binds to tumor necrosis factor-alpha (TNFα) and comprises:  
 XX (a) a heavy chain complementarily determining region 1 (CDR1) having the  
 XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 XX and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 XX (M1) the level of TNFα in a patient sample, comprising contacting with  
 XX (1), and detecting the level of binding between the antibody and TNFα in  
 XX the sample; (2) a composition comprising the antibody or its functional  
 XX fragment and a carrier; (3) treating (M2) an animal suffering from a  
 XX neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 XX animal in need of treatment for the disease by administering the human  
 XX monoclonal antibody of (I); and (4) inhibiting (M3) TNFα induced  
 XX apoptosis in an animal by selecting an animal in need of treatment for  
 XX TNFα induced apoptosis by administering the human monoclonal antibody of  
 XX (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,  
 XX antibacterial, antiinflammatory, antiproliferative, antirheumatic, eating-  
 XX disorder, immunomodulatory, immunosuppressive, nephroprotective,  
 XX neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 XX as a TNFα antagonist. The antibody (I) is useful in the preparation of  
 XX a medicament for treating TNF induced apoptosis, neoplastic disease such as  
 XX breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 XX stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 XX pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 XX diseases such as rheumatoid arthritis, glomerulonephritis,  
 XX atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 XX disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 XX multiple sclerosis. The present sequence represents a human anti-TNFα  
 XX antibody heavy chain variable region, which is used in the  
 XX exemplification of the present invention.  
 XX Sequence 128 AA;  
 XX  
 XX Query Match 83.2%; Score 511; DB 8; Length 128;  
 XX Best Local Similarity 78.9%; Pred. No. 7.9e-36;  
 XX Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;  
 QY 2 ESGGGLVPSQTLSTCTVSGSIRSGLYWSVRQPGKGLWIGNTYHSGNTYNPSTL 61  
 DB 6 ESGGGLVPSQTLSTCTVSGSIRSGLYWSVRQPGKGLWIGNTYHSGNTYNPSTL 65  
 QY 62 KSRITMSVDTSKRNHFSRLRTSVTAADTAAYVYCCARSDG-----YTLDMNGCGTLVVT 111  
 DB 66 KSRVTISVDTSKRNHFSRLRTSVTAADTAAYVYCCARSDG-----YTLDMNGCGTLVVT 125  
 QY 112 VSS 114  
 DB 126 VSS 128

AC ADP03982;  
 XX 29-JUL-2004 (first entry)  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.  
 XX  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 XX cytostatic; colorectal neoplasm; renal cell carcinoma;  
 XX cervical intraepithelial squamous neoplasia;  
 XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 XX gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX Unidentified.  
 XX WO2003048328-A2.  
 XX 12-JUN-2003.  
 XX 02-DEC-2002; 2002MO-US038550.  
 XX 03-DEC-2001; 2001US-0337275P.  
 XX (ABGE-) ABGENIX INC.  
 XX Gudae J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 XX intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX Example 2; SEQ ID NO 152; 89pp; English.  
 XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 XX comprising a heavy chain polypeptide and light chain polypeptide having a  
 XX sequence chosen from one of 53 fully defined amino acid sequences given  
 XX in the specification, where the antibody specifically binds carbonic  
 XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 XX demonstrates cytostatic activity and may be useful for treating a tumour,  
 XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 XX tumour or breast cancer, possibly via gene therapy. The current sequence  
 XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 XX (heavy chain variable domain) protein of the invention. The protein was  
 XX generated via the introduction of the human CA IX protein into a  
 XX transgenic mouse strain.  
 XX Sequence 121 AA;  
 XX  
 XX Query Match 83.1%; Score 510.5; DB 7; Length 121;  
 XX Best Local Similarity 82.8%; Pred. No. 8.2e-36;  
 XX Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;  
 QY 2 ESGGGLVPSQTLSTCTVSGSIRSGLYWSVRQPGKGLWIGNTYHSGNTYNPSTL 61  
 DB 6 ESGGGLVPSQTLSTCTVSGSIRSGLYWSVRQPGKGLWIGNTYHSGNTYNPSTL 65  
 QY 62 KSRITMSVDTSKRNHFSRLRTSVTAADTAAYVYCCARSDG-----GYTDMNGCGTLVWSS 114  
 DB 66 KSRVTISVDTSKRNHFSRLRTSVTAADTAAYVYCCARSDG-----GYTDMNGCGTLVWSS 121  
 RESULT 10  
 ID ADP03968  
 XX ADP03968 standard; protein; 118 AA.  
 XX ADP03968;  
 XX 29-JUL-2004 (first entry)  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.  
 XX

XX	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
OS	Unidentified.
PN	
XX	W02003046326-A2.
PD	
XX	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.
PI	
XX	Gudas J, Foltz I, Handa M, Gallo M;
XX	WPI; 2003-523295/49.
DR	
XX	
XX	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
XX	
PS	Example 2; SEQ ID NO 138; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated via the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	
SO	Sequence 118 AA;
XX	
Query Match	83.1%; Score 510; DB 7; Length 118;
Best Local Similarity	85.0%; Pred. No. 8.8e-36;
Matches	96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY	
DB	2 ESGGGLYKPESTSLILTCVSGGSIKSGYYSWVRQPKGLEMTGNHYHGNTYYNSL 61
DB	6 ESGGGLYKPESTSLILTCVSGGSIKSGYYSWVRQPKGLEMTGNHYHGNTYYNSL 65
QY	62 KSRITTSVDITSKNHFSLRLTSVTADPVAAYVCAISDGYTLDNMGCGTLVTYSS 114
DB	66 KSRITTSVDITSKNHFSLRLTSVTADPVAAYVCAISDGYTLDNMGCGTLVTYSS 118
RESULT 11	
ID	ADP03870 standard; protein; 123 AA.
XX	
AC	ADP03870;
DT	
XX	29-JUL-2004 (first entry)
DE	
XX	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	

OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Foltz I, Handa M, Gallo M;
XX	
DR	WPI; 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Claim 1; SEQ ID NO 10; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
XX	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cyrostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated by the introduction of the human CA IX protein into a
XX	transgenic mouse strain.
SQ	
XX	Sequence 123 AA:
Query Match	83.0%; Score 509.5; DB 7; Length 123;
Best Local Similarity	82.2%; Pred. No. 1e-35;
Matches	97; Conservative 8; Mismatches 8; Indels 5; Gaps 1,
OY	2 ESGGGLVKKPSQTLSLTCTVSCGSIRSGCYTWSWRPPGKLEMTIGNIYHSGNTYYNSL 61
DB	6 ESGGGLVKKPSQTLSLTCTVSCGSISGGGYMSWRHPGKGLEWIGIYYGSGSTYNSL 65
OY	62 KSRITMSVDTSIKNFESRLTFTVTADTAADVAVVYCARS-----DGYTLDMNGOGSTLVTVSS 114
DB	66 KSRYTIVSDTSIKNQPFLKLSSVTADTAADVVCARAGKYTGSGSYLDIWGOSTLVTVSS 123
RESULT 12	
ID	ADP03871
AC	ADP03871 standard; protein; 125 AA.
XX	
DT	ADP03871;
XX	
DT	29-JUN-2004 (first entry)
XX	
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein-SEQ 11.
XX	
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Foltz I, Handa M, Gallo M;
XX	
DR	WPI; 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Claim 1; SEQ ID NO 10; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
XX	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cyrostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated by the introduction of the human CA IX protein into a
XX	transgenic mouse strain.
SQ	
XX	Sequence 123 AA:
Query Match	83.0%; Score 509.5; DB 7; Length 123;
Best Local Similarity	82.2%; Pred. No. 1e-35;
Matches	97; Conservative 8; Mismatches 8; Indels 5; Gaps 1,
OY	2 ESGGGLVKKPSQTLSLTCTVSCGSIRSGCYTWSWRPPGKLEMTIGNIYHSGNTYYNSL 61
DB	6 ESGGGLVKKPSQTLSLTCTVSCGSISGGGYMSWRHPGKGLEWIGIYYGSGSTYNSL 65
OY	62 KSRITMSVDTSIKNFESRLTFTVTADTAADVAVVYCARS-----DGYTLDMNGOGSTLVTVSS 114
DB	66 KSRYTIVSDTSIKNQPFLKLSSVTADTAADVVCARAGKYTGSGSYLDIWGOSTLVTVSS 123
RESULT 12	
ID	ADP03871
AC	ADP03871 standard; protein; 125 AA.
XX	
DT	ADP03871;
XX	
DT	29-JUN-2004 (first entry)
XX	
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein-SEQ 11.
XX	
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;
KM	cervical intraepithelial squamous neoplasia;
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Foltz I, Handa M, Gallo M;
XX	
DR	WPI; 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Claim 1; SEQ ID NO 10; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
XX	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cyrostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

PF 02-DEC-2002; 2002MO-US038550.  
 XX  
 XX 03-DEC-2001; 2001US-0337275P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX  
 XX Gudäs J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 DR  
 XX  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Claim 1; SEQ ID NO 11; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosolic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 XX Sequence 125 AA;  
 SQ

Query Match 82.7%; Score 507.5; DB 7; Length 125;  
 Best Local Similarity 81.7%; Pred. No. 1.5e-35;  
 Matches 96; Conservative 7; Mismatches 8; Indels 7; Gaps 2;  
 QY 2 ESGPGLVKSQTLSTLCTVSGGSIRSGYWSWVROPKGLKLEWIGNIYHSGNTYNPSTL 61  
 DB 6 ESGPGLVKSQTLSTLCTVSGGSIRSGYWSWVROPKGLKLEWIGNIYHSGNTYNPSTL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCAR--DGY--TLDNMGCGTLVTVSS 114  
 DB 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCAR--DGY--TLDNMGCGTLVTVSS 125

RESULT 13  
 ADP03974  
 ID ADP03974 standard; protein; 120 AA.  
 XX  
 XX ADP03974;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
 XX  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 XX Unidentified.  
 OS  
 XX WO2003048328-A2.  
 PN  
 XX 12-JUN-2003.  
 PD  
 XX 02-DEC-2002; 2002MO-US038550.  
 PF  
 XX 03-DEC-2001; 2001US-0337275P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX

PI Gudäs J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 DR  
 XX  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Example 2; SEQ ID NO 144; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosolic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 XX Sequence 120 AA;  
 SQ

Query Match 82.6%; Score 507; DB 7; Length 120;  
 Best Local Similarity 83.6%; Pred. No. 1.6e-35;  
 Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;  
 QY 2 ESGPGLVKSQTLSTLCTVSGGSIRSGYWSWVROPKGLKLEWIGNIYHSGNTYNPSTL 61  
 DB 6 ESGPGLVKSQTLSTLCTVSGGSIRSGYWSWVROPKGLKLEWIGNIYHSGNTYNPSTL 65  
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCAR--DGY--TLDNMGCGTLVTVSS 114  
 DB 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCAR--DGY--TLDNMGCGTLVTVSS 120

RESULT 14  
 ADP03873  
 ID ADP03873 standard; protein; 120 AA.  
 XX  
 XX ADP03873;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 XX Unidentified.  
 OS  
 XX WO2003048328-A2.  
 PN  
 XX 12-JUN-2003.  
 PD  
 XX 02-DEC-2002; 2002MO-US038550.  
 PF  
 XX 03-DEC-2001; 2001US-0337275P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudäs J, Foltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 DR  
 XX  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 PS Claim 1; SEQ ID NO 13; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
 CC demonstrates cytotoxic activity and may be useful for treating a tumor,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumor or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX Sequence 120 AA;

Query Match 82.6%; Score 507; DB 7; Length 120;

Best Local Similarity 83.6%; Pred. No. 1.6e-35; Mismatches 7; Indels 4; Gaps 2;

Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;  
 QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYSGNTYYPSTL 61  
 DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYSGNTYYPSTL 65  
 QY 62 KSRITMSVDTSKNHSFLRLTSVTADTAVYYCARSDGVT--LDNKGQGLTVTVSS 114  
 DB 66 KSRVITISVDTSKNHSFLRLTSVTADTAVYYCAR--DGYNMYFDMGRGLTVTVSS 120

# RESULT 15

ADP03977  
 ID ADP03977 standard; protein; 122 AA.

XX ADP03977;  
 XX

XX 29-JUN-2004. (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.  
 DE  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumor antigen;  
 KW cytototoxic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002MO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudae J, Poltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX

XX Example 2; SEQ ID NO 147; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention  
 CC demonstrates cytotoxic activity and may be useful for treating a tumor,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumor or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX Sequence 122 AA;

Query Match 82.6%; Score 507; DB 7; Length 122;

Best Local Similarity 82.1%; Pred. No. 1.6e-35; Mismatches 9; Indels 4; Gaps 1;

Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;  
 QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYSGNTYYPSTL 61  
 DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYSWVRQPGKGLWIGNIYSGNTYYPSTL 65  
 QY 62 KSRITMSVDTSKNHSFLRLTSVTADTAVYYCAR--SDGYTLDMWGQGLTVTVSS 114  
 DB 66 KSRVITISVDTSKNHSFLRLTSVTADTAVYYCARYYDILTGMDVWGQGLTVTVSS 122

Search completed: August 30, 2006, 00:41:49  
 Job time : 103.427 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 / Search time 10.7091 Seconds  
(without alignments)  
1024.243 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 ESQGPGLVKSQTLSTLCTV.....RSDGYTLDMWGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 283416 seqe, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.5	81.4	135	2 S78051	Ig heavy chain pre
2	495.5	80.7	147	2 S13519	Ig heavy chain V r
3	487	79.3	130	2 S30534	Ig heavy chain V r
4	480.5	78.3	121	2 S44113	Ig heavy chain V r
5	478.5	77.9	140	2 I37782	Ig variable region
6	477.5	77.8	146	2 S09710	Ig heavy chain V r
7	474.5	77.3	116	2 S37456	Ig mu chain - huma
8	474.5	77.3	130	2 S31690	Ig heavy chain V r
9	474	77.2	122	2 S69912	Ig V-D-J region (N
10	473.5	77.1	128	2 S31514	Ig heavy chain - h
11	472.5	77.0	127	2 S19668	Ig heavy chain V r
12	469	76.4	137	2 S31676	Ig heavy chain V r
13	468.5	76.3	123	2 S30530	Ig heavy chain V r
14	465.5	75.8	155	2 S31511	Ig heavy chain - h
15	463.5	75.5	155	2 S31512	Ig heavy chain - h
16	462	75.2	139	2 S31586	Ig heavy chain V r
17	460.5	75.0	146	2 S09711	Ig heavy chain V r
18	460	74.9	145	2 S78055	Ig heavy chain pre
19	459.5	74.8	109	2 PH1673	Ig heavy chain V r
20	457	74.4	110	2 S44110	Ig heavy chain V-D
21	455	74.1	99	2 S26803	Ig heavy chain V r
22	454	73.9	139	2 A41287	Ig heavy chain pre
23	453	73.8	99	2 S26801	Ig heavy chain V r
24	452	73.6	129	2 S44114	Ig heavy chain V r
25	450	73.3	99	2 S26802	Ig heavy chain V r
26	450	73.3	135	2 S31604	Ig heavy chain V r
27	447	72.8	118	2 S20780	Ig heavy chain V r
28	446	72.6	99	2 S12418	Ig heavy chain V r
29	444.5	72.4	139	2 S31696	Ig heavy chain V r

30	443	72.1	118	2 A26340	Ig heavy chain pre
31	442.5	72.1	140	2 A49045	Ig heavy chain V r
32	441.5	71.9	132	2 A38911	Ig heavy chain V r
33	441	71.8	99	2 S26800	Ig heavy chain V r
34	441	71.8	126	2 S47010	Ig heavy chain V4.
35	440.5	71.7	129	2 D2H0A	Ig heavy chain V-I
36	440	71.7	97	2 PL0118	Ig heavy chain V-I
37	440	71.7	99	2 S26899	Ig heavy chain V r
38	439.5	71.6	98	2 S12421	Ig heavy chain V r
39	439.5	71.6	140	2 A24720	hypothetical hybr
40	439	71.5	140	2 S78052	Ig heavy chain pre
41	438.5	71.4	123	2 S30529	Ig heavy chain V r
42	438	71.3	120	2 PT0370	Ig mu chain precu
43	437	71.2	124	2 S31684	Ig heavy chain V r
44	435.5	70.9	134	2 S54906	Ig heavy chain V r
45	434.5	70.8	98	2 S26902	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

S78051  
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78051, S23716  
R/Harrindanath, N.  
Submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78051  
A/Molecule type: mRNA  
A/Residues: 1-135 <HAR>  
A/Cross-references: UNIPARC:UPI0000115887; EMBL:X54437; NID:937814; PIDN:CA38306.1; PID  
R/Harrindanath, N.; Goldfarb, I.S.; Ikematsu, H.; Butastero, S.E.; Wilder, R.L.; Norkins,  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hu  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23716  
A/Molecule type: mRNA  
A/Residues: 13-111 <HAM>  
A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F/1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F/14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F/27-111/Domain: immunoglobulin homology <IMM>  
Query Match 81.4%; Score 499.5; DB 2; Length 135;  
Best Local Similarity 79.7%; Pred. No. 1.1e-37;  
Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;  
Qy 2 ESQGPGLVKSQTLSTLCTVSGGSRGYYWVWPQKGLGEMIGNIYHSGNTYVPSL 61  
Db 18 ESQGPGLVKSQTLSTLCTVSGGSRGYYWVWPQKGLGEMIGNIYHSGNTYVPSL 77  
Qy 62 KSRITWSVTSKSKHFSRLTSVTAADTAIVYVYCAR--SDGYTLDM--WGGLTVTVSS 114  
Db 78 KSRITWSVTSKSKHFSRLTSVTAADTAIVYVYCAR--SDGYTLDM--WGGLTVTVSS 135  
RESULT 2  
S13519  
Ig heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S13519  
R/Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A/Reference number: S13519; MUID:91187691; PMID:2011536  
A/Accession: S13519

A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-147 <MOR>  
 A:Cross-references: UNIPARC:UPI0000115EB5; EMBL:X56158; NID:g37724; P1DN:CAA39626.1; P1D  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 495.5; DB 2; Length 147;  
 Best Local Similarity 80.2%; Pred. No. 2.7e-37;  
 Matches 93; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 61  
 DB 32 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 91

QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDG---DGYTLDMWGQGLTVTVSS 114  
 DB 92 KSRVTLSDVTSKNQFSLKLSVTADTAVYYCARPLMFGEPLFDYWGQGLTVTVSS 147

## RESULT 3

S30534  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
 C:Accession: S30534  
 R:Marlette, X.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S30520  
 A:Accession: S30534  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <MAR>

A:Cross-references: UNIPARC:UPI0000113P45; EMBL:Z18320  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 487; DB 2; Length 130;  
 Best Local Similarity 76.0%; Pred. No. 1.3e-36;  
 Matches 95; Conservative 7; Mismatches 11; Indels 12; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 61  
 DB 6 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDG-----YTLDMWGQGLTVTVSS 109  
 DB 66 KSRVTLSDVTSKNQFSLKLSVTADTAVYYCARDKGFWSGYTRNSRAAFDWGQGLTV 125

QY 110 VTVSS 114  
 DB 126 VTVSS 130

## RESULT 4

S44113  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
 C:Accession: S44113  
 R:Hawkins, R.B.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
 submitted to the EMBL Data Library, March 1994  
 A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A:Reference number: S44105  
 A:Accession: S44113  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-121 <HAM>  
 A:Cross-references: UNIPARC:UPI000011662F; EMBL:Z31389; NID:g472967; P1DN:CAA83264.1; P1D  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 480.5; DB 2; Length 121;  
 Best Local Similarity 78.4%; Pred. No. 4.7e-36;  
 Matches 91; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 61  
 DB 6 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDG---TLDWGQGLTVTVSS 114  
 DB 66 KSRVTLSDVTSKNQFSLKLSVTADTAVYYCARSLSGYSDPFDYWGQGLTVTVSS 121

## RESULT 5

I37782  
 Ig variable region (VDJ) (clone T23-9) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
 C:Accession: I37782; S25476  
 R:Demaison, C.; Chastagner, P.; There, J.; Zouali, M.  
 Proc. Natl. Acad. Sci. U.S.A. 91:514-518, 1994  
 A:Title: Somatic diversification in the heavy chain variable region genes expressed by h

A:Reference number: A36876; MUID:94119917; PMID:8290556  
 A:Accession: I37782  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <RES>  
 A:Cross-references: UNIPARC:UPI0000176E83; EMBL:X67906; NID:g33582; P1DN:CAA48104.1; P1D  
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 478.5; DB 2; Length 140;  
 Best Local Similarity 78.8%; Pred. No. 8.3e-36;  
 Matches 93; Conservative 9; Mismatches 9; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 61  
 DB 25 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 82

QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAVYYCARSDG---GYTLDMWGQGLTVTVSS 114  
 DB 83 KSRVTLSDVTSKNQFSLKLSVTADTAVYYCARHNSSSWGYRFPDYWGQGLTVTVSS 140

## RESULT 6

S09710  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S09710  
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwal, J.  
 Biochem. J. 268, 135-140, 1990  
 A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of

A:Reference number: S09710; MUID:90262535; PMID:2111699  
 A:Accession: S09710  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-146 <HUG>  
 A:Cross-references: UNIPARC:UPI000011586C; GB:X52110; NID:g31447; P1DN:CAA36344.1; P1D:g3  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 146;  
 Best Local Similarity 73.2%; Pred. No. 1.1e-35;  
 Matches 90; Conservative 13; Mismatches 9; Indels 11; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 61  
 DB 25 ESGPGLVKPSQTLSTLCVSGSIRSGYWSWVROPCKGLEWIGNIYHSGNTYNPSTL 84





A:Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterodimer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 463.5; DB 2; Length 155;  
Best Local Similarity 73.3%; Pred. No. 2e-34;  
Matches 88; Conservative 12; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGYYWVWVROPKGKLEWIGNIYHSGNTYYNPSTL 61  
Db 38 ESGPGLVKPSQTLSTCTVSGGSIKSGYYWVWVROPKGKLEWIGNIYHSGNTYYNPSTL 95  
QY 62 KSRITMSVITSKNHFSILRLTSVTADTAAYVYCARSDG-----YTLDMWGQGLTVVSS 114  
Db 96 KSRVITSVITSKNHFSILRLTSVTADTAAYVYCARSDG-----YTLDMWGQGLTVVSS 155

Search completed: August 30, 2006, 00:42:54  
Job time : 10.7091 sec

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 62.1818 Seconds  
(without alignments)  
1695.862 Million cell updates/sec

Title: US-10-027-725A-8  
Perfect score: 614  
Sequence: 1 IESGPGYVXPSTQLSLTCTV.....RSDGYLDMWGQGLTWTSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492.5	80.2	476	2	Q6GMX1_HUMAN
2	477	77.7	465	2	Q6GMX6_HUMAN
3	476.5	77.6	492	2	Q72374_HUMAN
4	470	76.5	478	2	Q72379_HUMAN
5	466	75.9	150	2	Q95973_HUMAN
6	466	75.9	196	2	Q96KX8_HUMAN
7	463.5	75.5	119	2	Q9UL73_HUMAN
8	457	74.4	477	2	Q6GMX7_HUMAN
9	457	74.4	620	2	Q96EY0_HUMAN
10	451	73.5	576	2	Q6PAI8_HUMAN
11	440.5	71.7	129	1	HV2F_HUMAN
12	429	69.9	130	2	Q81D7_HUMAN
13	427	69.5	139	2	Q86SX2_HUMAN
14	426.5	69.5	595	2	Q8WUX4_HUMAN
15	426.5	69.5	597	2	Q6GMX5_HUMAN
16	426.5	69.5	597	2	Q9BUI0_HUMAN
17	426.5	69.5	625	2	Q96AA6_HUMAN
18	422.5	68.8	597	2	Q9BQB8_HUMAN
19	417.5	68.0	478	2	Q6NYH3_HUMAN
20	417	67.9	146	1	HV2I_HUMAN
21	413	67.3	473	2	Q8TC63_HUMAN
22	386	62.9	116	2	Q723Y6_HUMAN
23	383.5	62.5	476	2	Q6MZX7_HUMAN
24	383	62.4	483	2	Q5U413_MOUSE
25	382.5	62.3	479	2	Q99M22_MOUSE
26	381.5	62.1	117	1	HV2G_HUMAN
27	377	61.4	136	2	Q6LBO5_MOUSE
28	375.5	61.2	615	2	Q569B6_RAT
29	371.5	60.5	477	2	Q510J1_RAT
30	365.5	59.5	119	2	Q53VR3_MOUSE
31	365	59.4	122	2	Q9UL75_HUMAN

32	363.5	59.2	137	1	HV46_MOUSE
33	360.5	58.7	115	2	Q53VQ1_MOUSE
34	360.5	58.7	262	2	Q56Z11_MOUSE
35	359.5	58.6	590	2	Q569B8_RAT
36	355.5	57.9	119	2	Q53VOS_MOUSE
37	355	57.8	485	2	Q56IMS_MOUSE
38	353	57.5	617	2	Q569B3_RAT
39	352.5	57.4	144	1	HV43_MOUSE
40	351	57.2	120	2	Q53VR7_MOUSE
41	347.5	56.6	113	1	HV47_MOUSE
42	347	56.5	591	2	Q510D9_RAT
43	346.5	56.4	121	2	Q9UL96_HUMAN
44	344.5	56.1	469	2	Q5M839_RAT
45	344.5	56.1	485	2	Q58E54_MOUSE

## ALIGNMENTS

RESULT 1  
Q6GMX1\_HUMAN PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 19-JUL-2004, integrated into UniProtKB/TREMBL.  
DT 19-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange S.J.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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CC  
CC EMBL: BC073773; AAH73773.1; mRNA.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG-cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR InterPro: IPR013106; V-set.  
DR Pfam: PF07654; C1-set; 3.

```

DR SMART: SM00409; IG: 1.
DR SMART: SM00407; IGC: 2.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PS50835; IG_LIKE: 4.
DR PROSITE: PS00290; IG_MSC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA562DDE9D CRC64;

Query Match          80.2%; Score 492.5; DB 2; Length 476;
Best Local Similarity 74.2%; Pred. No. 6,4e-42;
Matches 92; Conservative 13; Mismatches 6; Indels 13; Gaps 2

QY      2  ESGGGLVPSQTLSTCTVSGSGSIRSGSYMSWRQPGKGLIEWIGNITYHSGNTYYNDSL 61
Db      25  ESGGGLVPSQTLSTCTVSGSGSISGDIYMSWIMQPGKGLIEWIGITYHSGSITYNPSL 84
QY      62  KSRITMSVDTSKNHSRLSTVATADTVVYCARB-----DGYTLDMNGQGLTY 110
Db      85  KSRVITSLDTSKNPSLKNSTVADTVAVFYCARAGCWGSPFSAIDFENI--WGQITWV 142
QY      111 TVSS 114
Db      143 TVSS 146

RESULT 2
ID Q6GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
Nucleotide sequence.
TI TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schley G.D.,
RA Altschul S.F., Zeeberg B., Buco K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsten F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Liguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
Nucleotide sequence.
TI TISSUE=Primary B-Cells;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL: BC073766; AAH73766.1; -; mRNA.
DR InterPro: IPR003599; IG.

```

Query Match	Best Local Similarity	77.7%	Score 477;	DB 2;	Length 465;
Matches	92;	Conservative	81.4%;	6;	Mismatches 13;
				Indels	2;
				Gaps	1;
Qy	2	ESGGGLVYKPSQSTLSTCTTGGGSGTSSGCGYSSWNRQPPGGLEWINGIVHSGNRYNPSL	61		
Db	25	ESGGGLVYKPSSTLSTCTVSGGS--SGYSSWNRQPPAGGLEWINGIVHSGNRYNPSL	82		
Qy	62	KSRTTWSVDSIKNHFSLRLTSVTADTAVYVCAISDGYTLDMNGQGLTVYSS	114		
Db	83	KSRTTWSVDISIKNHFSLRLTSVTADTAVYVCAISDGYTLDMNGQGLTVYSS	135		
RESULT 3					
ID	Q72374 HUMAN	PRELIMINARY;	PRT;	492 AA.	
AC	Q72374				
DT	01-OCT-2003	integrated into UniProtKB/TrEMBL.			
DT	01-OCT-2003	sequence version 1.			
DT	07-FEB-2006	entry version 16.			
DE	Hypothetical protein DKFZp686C02218 (Fragment).				
GN	Name=DKFZp686C02218;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC	Homo.				
OX	NCEP	TaxID=9606;			
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	TISSUE=Human rectum tumor;				
RA	Bloecher H., Boeher M., Mewes H.W., Well B., Amlid C., Osanger A.,				
RA	Robo G., Han M., Wiemann S.;				
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.				
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>				
CC	Distributed under the Creative Commons Attribution-NonDerivs license				
CC	EMBL; BX538077; CAD98001.1; -, mRNA.				
DR	HSSP; P01820; 1G7J.				
DR	SMR; Q72374; 262-470.				
DR	InterPro; IPR003599; IG.				
DR	InterPro; IPR007110; IG_1like.				
DR	InterPro; IPR003597; IG_C1.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_V.				
DR	InterPro; IPR013106; V-set.				
DR	PIfam; PF07654; C1-set; 2.				
DR	SMART; SM00409; IG; 1.				
DR	SMART; SM00407; IGc1; 2.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS00835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.				
KW	Hypothetical protein				
SO	SEQUENCE	465 AA;	51083 MW;	B3A9B7D0FDB1386E	CRC64;



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QY 2 ESQPGLVKPSQTLSTCTVSGGSIIRSGYYSWVROPQKGLMIGNIYHSGNTYVPSL 61
DB 37 ESQPGLVKPSQTLSTCTVSGGSIIRSGYYSWVROPQKGLMIGNIYHSGNTYVPSL 96
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR---SDGYTLDMNGGTLTVVSS 114
DB 97 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCVRHVEGPGYGFDPWGQGTTLTVVSS 152

RESULT 4
QY 072379 HUMAN PRELIMINARY; PRT; 478 AA.
AC 072379;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wleemann S.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: BX538066; CA97996.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q72379; 248-456.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF0654; C1-set; 2.
DR SMART; SM00409; Ig_1.
DR SMART; SM00407; Ig_c1.
DR SMART; SM00406; Ig_v_1.
DR PROSITE; PS50835; Ig_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 76.5%; Score 470; DB 2; Length 478;
Best Local Similarity 75.7%; Pred. No. 1.3e-39;
Matches 87; Conservative 14; Mismatches 12; Indels 2; Gaps 1;

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DT 07-FEB-2006, entry version 23.
DE VH4 heavy chain variable region precursor (Fragment).
GN Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Behcet's patient with arthritis."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92031262; PubMed=1718404;
RA Harindranath N., Goldfarb I.S., Ikematsu H., Burastero S.B.,
RA Wilder R.L., Nockins A.L., Casali P.;
RT "Complete sequence of the genes encoding the VH and VL regions of low-
RT and high-affinity monoclonal IGM and IgA1 rheumatoid factors produced
RT by CD5+ B cells from a rheumatoid arthritis patient."
RL Int. Immunol. 3:865-875(1991).
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CC
CC EMBL: AF103795; AAC79084.1; -; mRNA.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; 1G7J.
DR SMR; O95973; 20-147.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; Ig_1.
DR SMART; SM00406; Ig_v_1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 20 >150 VH4 heavy chain variable region.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 150;
Best Local Similarity 76.1%; Pred. No. 9.5e-40;
Matches 86; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

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QY 2 ESQPGLVKPSQTLSTCTVSGGSIIRSGYYSWVROPQKGLMIGNIYHSGNTYVPSL 61
DB 24 ESQPGLVKPSQTLSTCTVSGGSIIRSGYYSWVROPQKGLMIGNIYHSGNTYVPSL 83
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGY--TLDMNGGTLTVVSS 114
DB 84 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSGVGLTAFDIMGGTLTVVSS 138

RESULT 5
QY 095973 HUMAN PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.

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RESULT 6
QY 096KX8 HUMAN PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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[illegible]

OC	Homo.	TaxID=9606;
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE:	
RX	MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;	
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Wysin-reactive autoantibodies in rheumatic carditis and normal fetus";	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE:	
RX	MEDLINE=92078875; PubMed=160528; DOI=10.1084/jem.174.6.1639;	
RA	Manheimer-Loy A., Katz J.B., Pillinger M., Grossein C., Smith A.,	
RA	Diamond B.;	
RT	"Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype";	
RL	J. Exp. Med. 174:1639-1652(1991).	
RN	[3]	
RP	NUCLEOTIDE SEQUENCE:	
RX	MEDLINE=90059975; PubMed=2511001;	
RA	Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;	
RT	"The smaller human VH gene families display remarkably little polymorphism.";	
RL	EMBO J. 8:3741-3748(1989).	
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CC	Distributed under the Creative Commons Attribution-NoDerivs License	
CC	-----	
DR	EMBL; AF035041; AAD56277.1; -; mRNA.	
DR	PIR; PH0876; PH0876.	
DR	PIR; S12416; S12416.	
DR	HSSP; P01820; 1G7J.	
DR	SMR; Q9UL73; 2-119.	
DR	LinkHub; Q9UL73; -;	
DR	InterPro; IPR003599; IG_1ike.	
DR	InterPro; IPR007110; IG_1like.	
DR	InterPro; IPR003596; IG_V.	
DR	InterPro; IPR013106; V-set.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
FT	Immunoglobulin domain.	
FT	NON_TER 1	
FT	NON_TER 1	
SO	SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;	
QY	Query Match 75.5%; Score 463.5; DB 2; Length 119;	
Db	Best Local Similarity 77.6%; Pred.No.1.3e-39;	
Matches	90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;	
QY	2 ESGPGLVPSQTSLTCTVGSGSIRSGGYSWVRPPPGKLEMGINIVHSGNTYPNSL 61	
Db	6 ESGPGLVPSSTLSLTCTVGSGSICS--YYWSWRPFGKLEWIGIYYSGSTNPSPSL 63	
QY	62 KSRITMSVDTSKNHESLRISVTAPDAVVYCAASDG---YTLDMOGCLTVTVSS 114	
Db	64 KSRVITSDRKSNQSLSLTILSIADPAVIFCARLSMWGPYFPDYGQGITLVSS 119	
RESULT 8		
ID	O6GMX7 HUMAN PRELIMINARY; PRT; 477 AA.	
AC	O6GMX7;	
DT	19-JUN-2004, integrated into UniProtKB/TrEMBL.	
DT	19-JUN-2004, sequence version 1.	
DE	07-FEB-2006, entry version 16.	
DI	Hypothetical protein.	
OS	Homo sapiens (Human) .	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;	
OX	Homo.	
OX	NCBI_TaxID=9606;	

RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Collins B., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: BC073765; AA073765.1; -; mRNA.  
 DR SMR: Q6GMX7; 247-455.  
 DR Ensemble: ENSG00000130076; Homo sapiens.  
 DR InterPro: IPR003593; IG.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07654; C1-set; 2.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00407; IGc1; 2.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9F59C09C50CF85 CRC64;  
 Query Match 74.4%; Score 457; DB 2; Length 477;  
 Best Local Similarity 77.4%; Pred. No. 2, 9e-38;  
 Matches 89; Conservative 7; Mismatches 15; Indels 4; Gaps 2;  
 Oy 2 ESGPGLVKSQTLSTLCTVSGSGSIRSGGYWVWVPPKGLWIGNIYHSGNTYNNPSL 61  
 Db 25 ESGPGLVKSQTLSTLCTVSGSGSIS--YVMSIRQTAGLWIGIYHSGSNTYNNPSL 82  
 Oy 62 KSRITNSVDTSKNHFSRLTSLTADTAAYVYCARSDG--YTLDDNGQGLTVTVSS 114  
 Db 83 KSRVTLSTLDTKQKQFSLRLNSVTADTAAYVYCAHSGSDWDFAFYWGQGLTVTVSS 137  
 RESULT 9  
 Q96EYO HUMAN PRELIMINARY; PRT; 620 AA.  
 AC Q96EYO;  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 2.  
 DT 07-FEB-2006, entry version 26.  
 DE IGm protein.  
 GN Name=IGM;

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 NC NCBITaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Collins B., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91252286; PubMed=1904154;  
 RA Neale G.A., Kitchingman G.R.;  
 RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
 chain enhancer region contain a non-translatable exon and are  
 RT extremely heterogeneous at the 5' end.";  
 RL Nucleic Acids Res. 19:2427-2433(1991).  
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 CC -----  
 DR EMBL: BC011857; AA11857.2; -; mRNA.  
 DR PIR: S15590; S15590.  
 DR HSSP: P01820; 1G7J.  
 DR SMR: Q96EYO; 27-251.  
 DR Ensemble: ENSG00000130076; Homo sapiens.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07654; C1-set; 4.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00407; IGc1; 3.  
 DR PROSITE: PS50835; IG\_LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_3.  
 SQ SEQUENCE 620 AA; 68125 MW; 99D01AA6B8F27B CRC64;  
 Query Match 74.4%; Score 457; DB 2; Length 620;  
 Best Local Similarity 78.0%; Pred. No. 3, 9e-38;  
 Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;  
 Oy 2 ESGPGLVKSQTLSTLCTVSGSGSIRSGGYWVWVPPKGLWIGNIYHSGNTYNNPSL 61  
 Db 32 ESGPGLVKSQTLSTLCTVSGSGSIS--YVMSIRQTAGLWIGIYHSGSNTYNNPSL 89

OY KSRITMSVDTSKNHFSLRTSVTADTAVYYCARSDGYTLDN-----WGQGLTVTVSS 114  
 DB 90 KSRVTVSVDTSKNHFSLRTSVTADTAVYYCARSDGYTLDN-----WGQGLTVTVSS 146

## RESULT 10

06P418\_HUMAN PRELIMINARY; PRT; 576 AA.  
 AC 06P418;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 21-FEB-2006, entry version 20.  
 DE IGH domain.  
 GN Name=IGHD;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dlatkovich L., Marinska K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tomihata S., Cavallini P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small J.D.,  
 RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
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 CC  
 CC EMBL, BC063384; AAH63384.1; -, mRNA.  
 DR HSSP, P01820; 1A7N.  
 DR Ensemble; ENSG00000196122; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR InterPro; IPR013151; Immunoglobulin.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
 SQ SEQUENCE 576 AA; 63364 MW; FBB97C949D720F1E CRC64;

Query Match 73.5%; Score 451; DB 2; Length 576;  
 Best Local Similarity 76.7%; Pred. No. 1,5e-37;  
 Matches 89; Conservative 7; Mismatches 16; Indels 4; Gaps 2;

OY 2 ESGPGLVKSQTLSTCTVSGGSIKSGYVWVROPKGLGEMIGNIVHSGNTYVPSL 61  
 DB 32 ESGPGLVKSQTLSTCTVSGGSIKSGYVWVROPKGLGEMIGNIVHSGNTYVPSL 90

OY 62 KSRITMSVDTSKNHFSLRTSVTADTAVYYCARSDG---YTLDNWGQGLTVTVSS 114  
 DB 91 KSRVTVSVDTSKNHFSLRTSVTADTAVYYCARSDGDIYYGMDVWGQGLTVTVSS 146

## RESULT 11

ID HV2F\_HUMAN STANDARD; PRT; 129 AA.  
 AC P01824;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 07-MAR-2006, entry version 36.  
 DE Ig heavy chain V-II region WH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=8222235; PubMed=6806818;  
 RA Takahashi N., Telaar D., Debure B., Lin L.-C., Putnam F.W.;  
 RT "Complete amino acid sequence of the delta heavy chain of human  
 RT immunoglobulin D.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
 CC -1- MISCELLANEOUS: This chain was isolated from an IgD myeloma  
 CC protein.  
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
 CC  
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 CC  
 CC PIR; A02099; D2HUMA.  
 DR PDB; 1ZVO; X-ray; C/D=.  
 DR SMR; P01824; 2-129.  
 DR GlycoSiteDB; P01824; -.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003623; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07654; V-set; 1.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;  
 KM Immunoglobulin V region.  
 FT CHAIN 1 >129  
 FT /FTID=PRO\_0000059912.  
 FT DOMAIN 1 113  
 FT NON\_TER 129 129  
 FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.7%; Score 440.5; DB 1; Length 129;  
 Best Local Similarity 65.1%; Pred. No. 3,4e-37;  
 Matches 82; Conservative 14; Mismatches 15; Indels 15; Gaps 2;

OY 2 ESGPGLVKSQTLSTCTVSGGSIKSGYVWVROPKGLGEMIGNIVHSGNTYVPSL 61  
 DB 6 ESGPGLVKSQTLSTCTVSGGSIKSGYVWVROPKGLGEMIGNIVHSGNTYVPSL 65

OY 62 KSRITMSVDTSKNHFSLRTSVTADTAVYYCARSDG---YTLDNWGQGLTVTVSS 108  
 DB 66 KSRVTVSVDTSKNHFSLRTSVTADTAVYYCARSDGDIYYGMDVWGQGLTVTVSS 123

OY 109 LTVTVSS 114

Db 124 TVHVS 129

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RESULT 12
Q81ZD7_HUMAN PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Anti-chyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jang Y.-J., Chung J.-Y., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY145445; AAN64329.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q81ZD7; 1-130.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin domain.
KW NON TER
FT 1
FT NON TER
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 69.3%; Score 429; DB 2; Length 130;
Best Local Similarity 68.8%; Pred. No. 5.2e-36;
Matches 86; Conservative 12; Mismatches 15; Indels 12; Gaps 4;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVROPCKGLEMIGNIYHSGNT-----Y 56
DB 6 QSGPGLVKPSQTLSTCTVSGSIRSGGYWVROPCKGLEMIGNIYHSGNT-----Y 56
QY 57 YNPSLKSRIYSDTSKXHFSLRLTSVTADTAADTAAYVYCAR----SDG--YT-LDNNCGQTL 109
DB 66 YAPSLSRVYISVDTSKXQSLSLSLSVTAADTAADTAAYVYCARFTHSGGCGYAFPGHKGQFL 125

QY 110 TVHVS 114
DB 126 TVHVS 130

RESULT 13
Q86SX2_HUMAN PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Full-length cDNA clone CSDD1004YW19 of B cells (Ramos cell line) of
DE Homo sapiens (human). (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BX248300; CAD62627.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q86SX2; 34-132.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT 1
FT NON TER
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 69.5%; Score 427; DB 2; Length 139;
Best Local Similarity 85.1%; Pred. No. 9.1e-36;
Matches 80; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVROPCKGLEMIGNIYHSGNTYNNPSL 61
DB 38 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVROPCKGLEMIGNIYHSGNTYNNPSL 61
QY 62 KSRITWSVDTSKXHFSLRLTSVTADTAADTAAYVYCAR 95
DB 96 KSRITWSVDTSKXQPSLKLSTVTAADTAADTAAYVYCAR 129

RESULT 14
Q8WDX4_HUMAN PRELIMINARY; PRT; 595 AA.
AC Q8WDX4;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 2.
DT 07-FEB-2006, entry version 24.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Mairia M.A.;

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OM protein - protein search, using SW model

Run on: August 30, 2006, 00:35:31 / Search time 15.5455 Seconds  
(without alignments)  
641.891 Million cell updates/sec

Title: US-10-027-725a-8

Perfect score: 614  
Sequence: 1 LBSPGLVVRSPQTLSTCTV.....RSDGYTLDMWGQGLTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patente\_AA:\*  
1: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5 COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6 COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7 COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/ECTUS COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/iaa/RE COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	82.6	473	2	US-09-049-672A-4
2	504.5	82.2	117	2	US-10-330-613A-13
3	494	80.5	122	1	US-08-360-125-11
4	494	80.5	122	1	US-08-450-578-11
5	494	80.5	122	1	US-09-017-628-11
6	494	80.5	122	1	US-09-014-880-11
7	494	80.5	122	2	US-08-450-363-11
8	494	80.5	122	2	US-09-467-903-11
9	494	80.5	172	2	US-09-472-087-7
10	494	80.5	172	2	US-09-472-087-86
11	493.5	80.4	117	2	US-10-330-613A-5
12	490.5	79.9	117	2	US-09-720-493-2
13	488.5	79.6	119	2	US-09-025-7698-39
14	488.5	79.6	119	2	US-09-025-7698-65
15	488.5	79.6	119	2	US-09-490-070A-39
16	488.5	79.6	119	2	US-09-490-070A-65
17	488.5	79.6	119	2	US-09-480-153-39
18	488.5	79.6	119	2	US-09-480-153-65
19	488.5	79.6	119	2	US-09-490-324-39
20	488.5	79.6	119	2	US-09-490-324-65
21	488	79.5	118	2	US-09-025-7698-25
22	488	79.5	118	2	US-09-490-070A-25
23	488	79.5	118	2	US-09-490-153-25
24	488	79.5	118	2	US-09-490-324-25
25	487.5	79.4	119	2	US-10-330-613A-25
26	482.5	78.6	121	2	US-10-330-613A-37

27	480.5	78.3	117	2	US-10-330-613A-33	Sequence 33, App1
28	478	77.9	487	2	US-09-800-729-145	Sequence 145, App1
29	477	77.7	180	2	US-09-424-840B-20	Sequence 20, App1
30	473.5	77.1	119	1	US-08-360-125-5	Sequence 5, App1
31	473.5	77.1	119	1	US-08-450-578-5	Sequence 5, App1
32	473.5	77.1	119	1	US-09-017-628-5	Sequence 5, App1
33	473.5	77.1	119	1	US-09-014-880-5	Sequence 5, App1
34	473.5	77.1	119	2	US-08-450-363-5	Sequence 5, App1
35	473.5	77.1	119	2	US-09-467-903-5	Sequence 5, App1
36	468.5	76.3	121	2	US-10-330-613A-9	Sequence 9, App1
37	467.5	76.1	121	2	US-10-330-613A-17	Sequence 17, App1
38	467.5	76.1	121	2	US-10-330-613A-17	Sequence 17, App1
39	459.5	74.8	142	1	US-08-480-774A-2	Sequence 2, App1
40	458	74.6	244	2	US-08-918-148-79	Sequence 79, App1
41	458	74.6	244	2	US-09-138-091A-77	Sequence 77, App1
42	455	74.1	99	2	US-10-194-975-38	Sequence 38, App1
43	454.5	74.0	125	2	US-10-432-006-1	Sequence 1, App1
44	454	73.9	230	2	US-10-194-975-110	Sequence 110, App1
45	453	73.8	99	2	US-10-194-975-36	Sequence 36, App1

ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049, 672A  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:



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LIBRARY: PANCYTUT01
CLONE: 1513264
US-09-049-672a-4

Query Match      82.6%; Score 507; DB 2; Length 473;
Best Local Similarity 79.8%; Pred. No. 1,1e-42;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGYVSWVRQPGKGLWIGNIYHSGNTYVNSL 61
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DB 25 ESGPGLVKSQTLSTCTVSGGSIIRSGYVSWVRQPGKGLWIGNIYHSGNTYVNSL 84

QY 62 KSRITNSVDTSKQHFSLRTSVTAADTAAYVYCARSD-----GYTLDNMGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 85 KSRVTTISVDTSKQFSLKLSVTADTAAYVYCARDDVGLRGNGYGMQVWGQGLTVTVSS 143

RESULT 2
US-10-330-613A-13
Sequence 13, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gludas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX, 022A
CURRENT APPLICATION NUMBER: US/10/330, 613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match      82.2%; Score 504.5; DB 2; Length 117;
Best Local Similarity 84.2%; Pred. No. 3.8e-43;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGYVSWVRQPGKGLWIGNIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKSQTLSTCTVSGGSIIRSGYVSWVRQPGKGLWIGNIYHSGNTYVNSL 65

QY 62 KSRITNSVDTSKQHFSLRTSVTAADTAAYVYCARSDGYTLDNMGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVTTISVDTSKQFSLKLSVTADTAAYVYCARDDVGLRGNGYGMQVWGQGLTVTVSS 117

RESULT 3
US-08-360-125-11
Sequence 11, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
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COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STRGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
CELL LINE: Hybridoma producing human antibody 1-3-1
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match      80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.5e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGYVSWVRQPGKGLWIGNIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKSQTLSTCTVSGGSIIRSGYVSWVRQPGKGLWIGNIYHSGNTYVNSL 65
```



QY 62 KSRITMSVPTSKNHFSLRLTSVTAADTAIVYYCARSD----GYTLDMWGQGLTVTVSS 114  
Db 66 KSRVITISVDTSKQFSLKLSVTAADTAIVYYCARSGSYGYYIGMDVWGQGLTVTVSS 122

## RESULT 4

US-08-450-578-11  
Sequence 11, Application US/08450578  
Patent No. 5837845  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Yoshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5837845hiko ITO  
APPLICANT: Kazuhito NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450, 578  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:

POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-11

Query Match 80.5%; Score 494; DB 1; Length 122;  
Best Local Similarity 78.6%; Pred. No. 4.5e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGYYWVWVPPGKGLMIGNIYHSGNTVYVPSL 61  
Db 6 ESGPGLVKSQTLSTCTVSGGSIIRSGYYWVWVPPGKGLMIGNIYHSGNTVYVPSL 65  
QY 62 KSRITMSVPTSKNHFSLRLTSVTAADTAIVYYCARSD----GYTLDMWGQGLTVTVSS 114  
Db 66 KSRVITISVDTSKQFSLKLSVTAADTAIVYYCARSGSYGYYIGMDVWGQGLTVTVSS 122

## RESULT 5

US-09-017-628-11  
Sequence 11, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Yoshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287hiko  
APPLICANT: NAGAIKE, Kazuhito  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1  
US-09-017-628-11

Query Match 80.5%; Score 494; DB 1; Length 122;  
Best Local Similarity 78.6%; Pred. No. 4.5e-42;  
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGYYWVWVPPGKGLMIGNIYHSGNTVYVPSL 61  
Db 6 ESGPGLVKSQTLSTCTVSGGSIIRSGYYWVWVPPGKGLMIGNIYHSGNTVYVPSL 65  
QY 62 KSRITMSVPTSKNHFSLRLTSVTAADTAIVYYCARSD----GYTLDMWGQGLTVTVSS 114  
Db 66 KSRVITISVDTSKQFSLKLSVTAADTAIVYYCARSGSYGYYIGMDVWGQGLTVTVSS 122

DB 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

## RESULT 6

US-09-014-880-11

; Sequence 11, Application US/09014880  
; Patent No. 5990297

## GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA et al.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind &amp; Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/014,880

FILING DATE: January 28, 1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/450,578

FILING DATE: May 25, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125

FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

US-09-014-880-11

Query Match 80.5%; Score 494; DB 1; Length 122;

Best Local Similarity 78.6%; Pred. No. 4.5e-42;

Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Db 2 EBSGPGVLPKPSQTLSTCTVSGSIRSGGYTWSWVQPPGKGLWGNIGYHSGNTYVNSL 61

Db 6 EBSGPGVLPKPSQTLSTCTVSGSIRSGGYTWSWVQPPGKGLWGNIGYHSGNTYVNSL 65

Qy 62 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSD---GYTLDWGGGTLTVVSS 114

Qy 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

Db 66 KSRVTVSDTSKNGFSLKLSVTADTAAYVYCARSGSYGGYYGMDVWGQTTVTVSS 122

## GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA

APPLICANT: Yoshiaki TAGAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: No. 643634/Iniko ITO

APPLICANT: Kazuhiko NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind &amp; Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,363

FILING DATE: May 25, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125

FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human antibody 1-3-1

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

```

/      AUTHORS:
/      TITLE:
/      JOURNAL:
/      VOLUME:
/      ISSUE:
/      PAGES:
/      DATE:
/      DOCUMENT NUMBER:
/      FILING DATE:
/      PUBLICATION DATE:
/      RELEVANT RESIDUES IN SEQ ID NO:
/
US-08-450-363-11

Query Match      80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.5e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY      2  ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWSWVROPKGLWIGNIYHSGNTYNPSTL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWSWVROPKGLWIGNIYHSGNTYNPSTL 65
QY      62 KSRVTISVDTSKNQSRLTSVTAADTAVYYCARSD---GYLDMWGQGLTVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66 KSRVTISVDTSKNQSRLTSVTAADTAVYYCARSGSYGYGYGMDVWGQGLTVTVSS 122

RESULT 8
US-09-467-903-11
/      Sequence 11, Application US/09467903
/      Patent No. 6787153
/      GENERAL INFORMATION:
/      APPLICANT: Saijo HOSOKAWA
/      Yoshiaki TAGAWA
/      Yoko HIRAKAWA
/      No. 6787153ihiko ITO
/      Kazuhiko NAGAIKE
/      TITLE OF INVENTION: Human Monoclonal Antibody
/      Specifically Binding to Surface Antigen of Cancer
/      Cell Membrane
/
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,363
FILING DATE: May 25, 1995
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER: JP158859/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158861/1991
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>

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/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: 202-721-8200
/      TELEFAX: <Unknown>
/      TELEX: <Unknown>
/      INFORMATION FOR SEQ ID NO: 11:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 122 amino acids
/      TYPE: amino acid
/      STRANDEDNESS: single
/      TOPOLOGY: linear
/      MOLECULE TYPE: protein
/      HYPOTHETICAL: <Unknown>
/      ANTI-SENSE: <Unknown>
/      ORIGINAL SOURCE:
/      ORGANISM: <Unknown>
/      STRAIN: <Unknown>
/      INDIVIDUAL ISOLATE: <Unknown>
/      DEVELOPMENTAL STAGE: <Unknown>
/      HAPLOTYPE: <Unknown>
/      TISSUE TYPE: <Unknown>
/      CELL TYPE: Hybridoma producing human antibody 1-3-1
/      CELL LINE: <Unknown>
/      ORGANELL: <Unknown>
/      IMMEDIATE SOURCE:
/      LIBRARY: <Unknown>
/      CLONE: <Unknown>
/      POSITION IN GENOME:
/      CHROMOSOME/SEGMENT: <Unknown>
/      MAP POSITION: <Unknown>
/      UNITS: <Unknown>
/      FEATURE:
/      NAME/KEY:
/      LOCATION:
/      IDENTIFICATION METHOD:
/      OTHER INFORMATION:
/      PUBLICATION INFORMATION:
/      AUTHORS:
/      TITLE:
/      JOURNAL:
/      VOLUME:
/      ISSUE:
/      PAGES:
/      DATE:
/      DOCUMENT NUMBER:
/      FILING DATE:
/      PUBLICATION DATE:
/      RELEVANT RESIDUES IN SEQ ID NO:
/      SEQUENCE DESCRIPTION: SEQ ID NO: 11:
/
US-09-467-903-11

Query Match      80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.5e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY      2  ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWSWVROPKGLWIGNIYHSGNTYNPSTL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWSWVROPKGLWIGNIYHSGNTYNPSTL 65
QY      62 KSRVTISVDTSKNQSRLTSVTAADTAVYYCARSD---GYLDMWGQGLTVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66 KSRVTISVDTSKNQSRLTSVTAADTAVYYCARSGSYGYGYGMDVWGQGLTVTVSS 122

RESULT 9
US-09-472-087-7
/      Sequence 7, Application US/09472087
/      Patent No. 6682736
/      GENERAL INFORMATION:
/      APPLICANT: HANSON, DOUGLAS C.
/      APPLICANT: NEVEU, MARK J.
/      APPLICANT: MUELLER, EILEEN E.
/      APPLICANT: HANKE, JEFFREY H.
/      APPLICANT: GILMAN, STEVEN C.

```

```

; APPLICANT: DAVIS, C. GEOFFREY
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      80.5%; Score 494; DB 2; Length 172;
Best Local Similarity 81.6%; Pred. No. 6,7e-42;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;
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Qy 3 SGGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 62
Db 1 SGGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 60
Qy 63 SRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDMWGQGLTVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSVTAADTAVYYCARSDGSDYGIIDVWGQGLTVTVSS 114
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RESULT 10
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALLAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86
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Query Match      80.5%; Score 494; DB 2; Length 172;
Best Local Similarity 81.6%; Pred. No. 6,7e-42;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

Qy 3 SGGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 62
Db 1 SGGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 60
Qy 63 SRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG--YTLDMWGQGLTVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSVTAADTAVYYCARSDGSDYGIIDVWGQGLTVTVSS 114
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RESULT 11
US-10-330-613A-5
; Sequence 5, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
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; APPLICANT: Guigas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-5
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Query Match      80.4%; Score 493.5; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 4.8e-42;
Matches 95; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

Qy 2 ESGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 61
Db 6 ESGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR--SDGTTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARSDGDKYK--WGQGLTVTVSS 117
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RESULT 12
US-09-720-493-2
; Sequence 2, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Holte, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Darmanis, Olayekan
; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHB/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-720-493-2
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Query Match      79.9%; Score 490.5; DB 2; Length 117;
Best Local Similarity 81.4%; Pred. No. 9.6e-42;
Matches 92; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 2 ESGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 61
Db 6 ESGPLVKSQTLSTCTVSGSIRSGYVSWVRQPGKLEWIGNTYHSGNTYVNSLK 64
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGTTLDNWGQGLTVTVSS 114
Db 65 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARSKMSKRDYWGQGLTVTVSS 117
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RESULT 13
US-09-025-769B-39
; Sequence 39, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
```

APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
TITLE OF INVENTION: Plueckhuhn, Andreas  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9090  
TELEFAX: (212)596-9000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-39  
Query Match 79.6%; Score 488.5; DB 2; Length 119;  
Best Local Similarity 81.9%; Pred. No. 1.5e-41;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVWVRPPGKGLMIGNIYHSGNTYNPSTL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYVWVRPPGKGLMIGNIYHSGNTYNPSTL 63  
QY 62 KSRITVSDTSKXHFSLRLTSVTAADTAVYYCAR--SDG-YTLDNMGQGLTVTVSS 114  
DB 64 KSRVITSDTSKXHFSLRLTSVTAADTAVYYCARWGDDGFYADYMGQGLTVTVSS 119  
RESULT 14  
US-09-025-769B-65  
Sequence 65, Application US/09025769B  
Patent No. 6300664  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
TITLE OF INVENTION: Plueckhuhn, Andreas  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9090  
TELEFAX: (212)596-9000  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65  
Query Match 79.6%; Score 488.5; DB 2; Length 119;  
Best Local Similarity 81.9%; Pred. No. 1.5e-41;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;  
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVWVRPPGKGLMIGNIYHSGNTYNPSTL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYVWVRPPGKGLMIGNIYHSGNTYNPSTL 63  
QY 62 KSRITVSDTSKXHFSLRLTSVTAADTAVYYCAR--SDG-YTLDNMGQGLTVTVSS 114  
DB 64 KSRVITSDTSKXHFSLRLTSVTAADTAVYYCARWGDDGFYADYMGQGLTVTVSS 119  
RESULT 15  
US-09-490-070A-39  
Sequence 39, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
TITLE OF INVENTION: Plueckhuhn, Andreas  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McCulliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:

```
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39

Query Match          79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.5e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

QY      2  ESGGGLVKEPSQTLSTCTVSGGSTRSGGYKSWVRQPPGKGLWIGNIYHSGNTYVNPSTL 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      6  ESGGGLVKEPSQTLSTCTVSGGSTRSGGYKSWVRQPPGKGLWIGNIYHSGNTYVNPSTL 63

QY      62  KSRITMSVDTSKNHPSRLTSVTADTAIVYYCAR--SDG-YTLDDMGQGLTVTVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      64  KSRVTISVDTSKNHPSRLTSVTADTAIVYYCARMGGDGFYAMDYWGQGLTVTVSS 119
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Search completed: August 30, 2006, 00:37:09  
Job time : 15.5455 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 65.2909 Seconds  
(without alignments)  
808.788 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLTVTS 114Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	4	US-10-027-725A-8
2	600	97.7	114	4	US-10-027-725A-9
3	546	88.9	114	4	US-10-027-725A-7
4	514.5	83.8	140	5	US-10-893-576-41
5	511	83.2	128	5	US-10-727-155-2
6	511	83.2	128	5	US-10-727-155-10
7	511	83.2	128	5	US-10-727-155-30
8	510.5	83.1	121	4	US-10-309-762-152
9	510	83.1	118	4	US-10-309-762-138
10	509.5	83.0	123	4	US-10-309-762-10
11	507.5	82.7	125	4	US-10-309-762-11
12	507	82.6	120	4	US-10-309-762-13
13	507	82.6	120	4	US-10-309-762-144
14	507	82.6	122	4	US-10-309-762-147
15	506.5	82.5	119	5	US-10-893-576-189
16	506	82.4	221	3	US-09-972-656-80
17	505.5	82.3	121	4	US-10-309-762-151
18	505	82.2	128	5	US-10-727-155-26
19	504.5	82.2	117	4	US-10-330-613-13
20	504.5	82.2	117	4	US-10-330-613-13
21	504.5	82.2	117	4	US-10-660-357-13
22	504	82.1	121	5	US-10-805-177-56
23	503.5	82.0	119	4	US-10-309-762-140
24	503.5	82.0	148	6	US-11-131-648-13
25	503.5	82.0	148	6	US-11-131-648-35
26	503	81.9	125	5	US-10-805-177-53
27	502.5	81.8	123	4	US-10-309-762-12

28	502.5	81.8	144	5	US-10-893-576-35	Sequence 35, Appl
29	502	81.8	122	5	US-10-984-960A-56	Sequence 56, Appl
30	502	81.8	124	5	US-10-309-762-75	Sequence 75, Appl
31	502	81.8	143	4	US-10-309-762-96	Sequence 96, Appl
32	501	81.6	130	6	US-11-009-731-46	Sequence 46, Appl
33	501	81.6	222	3	US-09-880-748-1329	Sequence 1329, Ap
34	501	81.6	252	4	US-10-293-418-1329	Sequence 1329, Ap
35	501	81.6	252	6	US-11-054-515-1329	Sequence 1329, Ap
36	501	81.6	252	6	US-11-054-515-1329	Sequence 1329, Ap
37	500	81.4	120	4	US-10-309-762-128	Sequence 128, Ap
38	500	81.4	120	4	US-10-309-762-139	Sequence 139, Ap
39	500	81.4	121	4	US-10-308-817-137	Sequence 137, Ap
40	500	81.4	121	4	US-10-453-698-137	Sequence 137, Ap
41	500	81.4	126	5	US-09-974-449-6	Sequence 6, Appl
42	500	81.4	126	5	US-10-652-502A-18	Sequence 18, Appl
43	499.5	81.4	135	4	US-10-388-214A-34	Sequence 34, Appl
44	499	81.3	116	4	US-10-309-762-127	Sequence 127, Appl
45	499	81.3	120	5	US-10-706-689-40	Sequence 40, Appl

## ALIGNMENTS

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RESULT 1
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-8

Query Match      100.0%; Score 614; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 9, 3e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYMSWVQPPGKGLWIGNIYHSGNTYVPS 60
      |||
DB      1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYMSWVQPPGKGLWIGNIYHSGNTYVPS 60
      |||

QY      61 LKSRITMSVDTSKNHSRLTSTADTAVYYCARSDGYTLDMWGQGLTVTS 114
      |||
DB      61 LKSRITMSVDTSKNHSRLTSTADTAVYYCARSDGYTLDMWGQGLTVTS 114
      |||

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-027-725A-9

Query Match 97.7%; Score 600; DB 4; Length 114;  
Best Local Similarity 96.5%; Pred. No. 1,7e-46;  
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LBSGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPS 60  
DB 1 LBSGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPS 60  
QY 61 LKSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
DB 61 LKSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

## RESULT 3

US-10-027-725A-7  
Sequence 7, Application US/10027725A  
Publication No. US20030082659A1

GENERAL INFORMATION:  
APPLICANT: Flicker, Sabine  
TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof  
FILE REFERENCE: 25401-4  
CURRENT APPLICATION NUMBER: US/10/027,725A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/259,436  
PRIOR FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-027-725A-7

Query Match 88.9%; Score 546; DB 4; Length 114;  
Best Local Similarity 89.5%; Pred. No. 1,3e-41;  
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 LBSGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPS 60  
DB 1 LBSGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPS 60  
QY 61 LKSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
DB 61 LKSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

## RESULT 4

US-10-893-576-41  
Sequence 41, Application US/10893576  
Publication No. US20050118643A1

GENERAL INFORMATION:  
APPLICANT: BURGESS, TERESA L.  
APPLICANT: COXON, ANGELA  
APPLICANT: GREEN, LARRY L.  
APPLICANT: ZHANG, KE  
TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCTYTE GROWTH FACTOR  
FILE REFERENCE: 06843.0051-00000  
CURRENT APPLICATION NUMBER: US/10/893,576  
CURRENT FILING DATE: 2004-07-16  
PRIOR APPLICATION NUMBER: US 60/488,681  
PRIOR FILING DATE: 2003-07-18  
NUMBER OF SEQ ID NOS: 194  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 41  
LENGTH: 140

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 2,40.1  
OTHER INFORMATION: Heavy chain V region (Vh, Vg 4-31)-huIG2 C region

US-10-893-576-41

Query Match 83.8%; Score 514.5; DB 5; Length 140;  
Best Local Similarity 84.5%; Pred. No. 1,1e-38;  
Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPSL 61  
DB 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPSL 84  
QY 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114  
DB 85 KSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 140

## RESULT 5

US-10-727-155-2  
Sequence 2, Application US/10727155  
Publication No. US20050049402A1

GENERAL INFORMATION:  
APPLICANT: John S. Babcock  
APPLICANT: Jaspal S. Kang  
APPLICANT: Orit Foord  
APPLICANT: Larry Green  
APPLICANT: Xiao Feng  
APPLICANT: Scott Kikamp  
APPLICANT: Mary Haak-Frendscho  
APPLICANT: Palaniswami Rathanaswami  
APPLICANT: Craig Pigott  
APPLICANT: Meina Liang  
APPLICANT: Rozanne Lee  
APPLICANT: Kathy Manchulench  
APPLICANT: Raffaella Faggioni  
APPLICANT: Giorgio Senaldi  
APPLICANT: Qiaojuan Jane Su  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
FILE REFERENCE: ABGENIX.073A  
CURRENT APPLICATION NUMBER: US/10/727,155  
CURRENT FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/430729  
PRIOR FILING DATE: 2002-12-02  
NUMBER OF SEQ ID NOS: 320  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-727-155-2

Query Match 83.2%; Score 511; DB 5; Length 128;  
Best Local Similarity 78.9%; Pred. No. 2,1e-38;  
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYMSWROPKGLGEMIGNIYHSGNTYNNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDG-----YTLDMWGQGLTVT 111  
DB 66 KSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCARSDG-----YTLDMWGQGLTVT 125  
QY 112 VSS 114  
DB 126 VSS 128

## RESULT 6

US-10-727-155-10  
Sequence 10, Application US/10727155  
Publication No. US20050049402A1

GENERAL INFORMATION:  
APPLICANT: John S. Babcock



```
/ APPLICANT: Jaapal S. Kang
/ APPLICANT: Orit Fecord
/ APPLICANT: Larry Green
/ APPLICANT: Xiao Feng
/ APPLICANT: Scott Klakamp
/ APPLICANT: Mary Haak-Frendescho
/ APPLICANT: Palaniswami Rathanaswami
/ APPLICANT: Craig Figgott
/ APPLICANT: Meina Liang
/ APPLICANT: Rozanne Lee
/ APPLICANT: Kathy Manchulenko
/ APPLICANT: Raffaela Faggioni
/ APPLICANT: Giorgio Senaldi
/ APPLICANT: Qiaojuan Jane Su
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
/ TITLE OF INVENTION: FACTOR AND USES THEREOF
/ FILE REFERENCE: ABGENIX.073A
/ CURRENT APPLICATION NUMBER: US/10/727,155
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR FILING DATE: 2002-12-02
/ NUMBER OF SEQ ID NOS: 320
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-727-155-10
```

```
Query Match 83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 2.1e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGGYWMSVRQPKGLWIGNIYSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCVSGSIRSGGYWMSVRQPKGLWIGNIYSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTAVYYCARSDG-----YTLDMNGGGLTVT 111
DB 66 KSRVITISVDTSKNPSLKLSTVTAADTAVYYCARSDNQNMNDEVYDGLDVGGGTTVT 125
```

```
QY 112 VSS 114
DB 126 VSS 128
```

## RESULT 7

```
US-10-727-155-30
/ Sequence 30, Application US/10727155
/ Publication No. US20050049402A1
/ GENERAL INFORMATION:
/ APPLICANT: John S. Babcock
/ APPLICANT: Jaapal S. Kang
/ APPLICANT: Orit Fecord
/ APPLICANT: Larry Green
/ APPLICANT: Xiao Feng
/ APPLICANT: Scott Klakamp
/ APPLICANT: Mary Haak-Frendescho
/ APPLICANT: Palaniswami Rathanaswami
/ APPLICANT: Craig Figgott
/ APPLICANT: Meina Liang
/ APPLICANT: Rozanne Lee
/ APPLICANT: Kathy Manchulenko
/ APPLICANT: Raffaela Faggioni
/ APPLICANT: Giorgio Senaldi
/ APPLICANT: Qiaojuan Jane Su
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
/ TITLE OF INVENTION: FACTOR AND USES THEREOF
/ FILE REFERENCE: ABGENIX.073A
/ CURRENT APPLICATION NUMBER: US/10/727,155
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/430729
/ PRIOR FILING DATE: 2002-12-02
```

```
/ NUMBER OF SEQ ID NOS: 320
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-727-155-30
```

```
Query Match 83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 2.1e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGGYWMSVRQPKGLWIGNIYSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCVSGSIRSGGYWMSVRQPKGLWIGNIYSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTAVYYCARSDG-----YTLDMNGGGLTVT 111
DB 66 KSRVITISVDTSKNPSLKLSTVTAADTAVYYCARSDNQNMNDEVYDGLDVGGGTTVT 125
```

```
QY 112 VSS 114
DB 126 VSS 128
```

## RESULT 8

```
US-10-309-762-152
/ Sequence 152, Application US/10309762
/ Publication No. US20040018198A1
/ GENERAL INFORMATION:
/ APPLICANT: Gudas, Jean
/ APPLICANT: Folz, Ian
/ APPLICANT: Handa, Masahisa
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
/ FILE REFERENCE: ABGENIX.027A
/ CURRENT APPLICATION NUMBER: US/10/309,762
/ PRIOR FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: 60/337275
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 152
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-309-762-152
```

```
Query Match 83.1%; Score 510.5; DB 4; Length 121;
Best Local Similarity 82.8%; Pred. No. 2.2e-38;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTLCVSGSIRSGGYWMSVRQPKGLWIGNIYSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTLCVSGSIRSGGYWMSVRQPKGLWIGNIYSGNTYNNPSL 65
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTAVYYCARSD---GYTLDMNGGGLTVT 114
DB 66 KSRVITISVDTSKNPSLKLSTVTAADTAVYYCAVDILGVAFDILWGGGTTVT 121
```

## RESULT 9

```
US-10-309-762-138
/ Sequence 138, Application US/10309762
/ Publication No. US20040018198A1
/ GENERAL INFORMATION:
/ APPLICANT: Gudas, Jean
/ APPLICANT: Folz, Ian
/ APPLICANT: Handa, Masahisa
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
/ TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

```
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138
```

```
Query Match      83.1%; Score 510; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 2,4e-38;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGTYLDNMGCGTLVTVSS 114
Db 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARVYSGSDYWGQGLVTVSS 118
```

## RESULT 10

```
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Handa, Masahisa
; APPLICANT: Foltz, Ian
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
```

```
Query Match      83.0%; Score 509.5; DB 4; Length 123;
Best Local Similarity 82.2%; Pred. No. 2,7e-38;
Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGTYLDNMGCGTLVTVSS 114
Db 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARAGKRYGSGYLDYWGQGLVTVSS 123
```

## RESULT 11

```
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
```

```
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11
```

```
Query Match      82.7%; Score 507.5; DB 4; Length 125;
Best Local Similarity 81.7%; Pred. No. 4,2e-38;
Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGTYLDNMGCGTLVTVSS 114
Db 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARVYDFLTGYPAFDIMGQGLVTVSS 125
```

## RESULT 12

```
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13
```

```
Query Match      82.6%; Score 507; DB 4; Length 120;
Best Local Similarity 83.6%; Pred. No. 4,5e-38;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
```

```
QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGGYWVWROPKGLEWIGNIYHSGNTYYPSTL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGTYLDNMGCGTLVTVSS 114
Db 66 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGTYLDNMGCGTLVTVSS 120
```

## RESULT 13

```
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
```

;; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
;; FILE REFERENCE: (CA IX) TUMOR ANTIGEN  
;; CURRENT APPLICATION NUMBER: US/10/309,762  
;; PRIOR FILING DATE: 2002-12-02  
;; PRIOR FILING DATE: 2001-12-03  
;; NUMBER OF SEQ ID NOS: 246  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 144  
;; LENGTH: 120  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-309-762-144

Query Match 82.6%; Score 507; DB 4; Length 120;  
Best Local Similarity 83.6%; Pred. No. 4.5e-38;  
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVROPFGKLEWIGNIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWIRQHPGKLEWIGNIYHSGNTYNNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAAYYCARSDGYT---LDNMGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYYCAR-DCYNYWYFDLWGGTLTVTVSS 120

RESULT 14  
US-10-309-762-147  
;; Sequence 147, Application US/10309762  
;; Publication No. US20040018198A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gudas, Jean  
;; APPLICANT: Foltz, Ian  
;; APPLICANT: Handa, Masahisa  
;; APPLICANT: Gallo, Michael  
;; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
;; FILE REFERENCE: ABGENIX.027A  
;; CURRENT APPLICATION NUMBER: US/10/309,762  
;; CURRENT FILING DATE: 2002-12-02  
;; PRIOR FILING DATE: 2001-12-03  
;; NUMBER OF SEQ ID NOS: 246  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 147  
;; LENGTH: 122  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-309-762-147

Query Match 82.6%; Score 507; DB 4; Length 122;  
Best Local Similarity 82.1%; Pred. No. 4.5e-38;  
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVROPFGKLEWIGNIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWIRQHPGKLEWIGNIYHSGNTYNNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAAYYCAR---SDGYTLDMNGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYYCARYYDILTGMDWDWGQGLTVTVSS 122

RESULT 15  
US-10-893-576-189  
;; Sequence 189, Application US/10893576  
;; Publication No. US20050118643A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BURGESS, TERESA L.  
;; APPLICANT: COXON, ANGELA  
;; APPLICANT: GREEN, LARRY L.

;; APPLICANT: ZHANG, KE  
;; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR  
;; FILE REFERENCE: 06843.0051-00000  
;; CURRENT APPLICATION NUMBER: US/10/893,576  
;; PRIOR FILING DATE: 2004-07-16  
;; PRIOR FILING DATE: 2003-07-18  
;; NUMBER OF SEQ ID NOS: 194  
;; SOFTWARE: PatentIn Ver. 3.2  
;; SEQ ID NO 189  
;; LENGTH: 119  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic gamma heavy  
US-10-893-576-189

Query Match 82.5%; Score 506.5; DB 5; Length 119;  
Best Local Similarity 84.2%; Pred. No. 4.9e-38;  
Matches 96; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWVROPFGKLEWIGNIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGSIRSGYYMSWIRQHPGKLEWIGNIYHSGNTYNNPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTADTAAYYCARSDGYT---LDNMGQGLTVTV 112  
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYYCAR-DCYNYWYFDLWGGTLTVTV 119

Search completed: August 30, 2006, 00:50:39  
Job time : 66.2909 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 13.4727 Seconds  
(without alignments)  
578.960 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614  
Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLTVVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications AA New:  
1: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US09\_NEW\_PUB.pep.\*  
2: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US06\_NEW\_PUB.pep.\*  
3: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US07\_NEW\_PUB.pep.\*  
4: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US08\_NEW\_PUB.pep.\*  
5: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/PCT\_NEW\_PUB.pep.\*  
6: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US10\_NEW\_PUB.pep.\*  
7: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US11\_NEW\_PUB.pep.\*  
8: /IMC\_Celerra\_SIDS3/prodata/2/pubppa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510.5	83.1	118	6	US-10-981-300-51 Sequence 51, App1
2	488.5	79.6	119	7	US-11-304-986-25 Sequence 25, App1
3	487.5	79.4	149	7	US-11-355-464-13 Sequence 13, App1
4	487.5	79.4	149	7	US-11-355-464-16 Sequence 16, App1
5	485.5	79.1	118	6	US-10-981-300-52 Sequence 52, App1
6	485.5	79.1	180	6	US-10-981-300-4 Sequence 4, App1
7	483.5	78.7	121	7	US-11-337-300-84 Sequence 84, App1
8	483.5	78.7	248	7	US-11-337-300-94 Sequence 94, App1
9	481.5	78.4	121	7	US-11-211-917-82 Sequence 82, App1
10	481.5	78.4	121	7	US-11-211-917-98 Sequence 98, App1
11	481.5	78.4	466	7	US-11-211-917-70 Sequence 70, App1
12	481.5	78.4	466	7	US-11-211-917-86 Sequence 86, App1
13	479.5	78.1	121	7	US-11-211-917-66 Sequence 66, App1
14	478	77.9	118	7	US-11-211-917-109 Sequence 109, App1
15	478	77.9	118	7	US-11-211-917-142 Sequence 142, App1
16	478	77.9	120	7	US-11-281-266-6 Sequence 6, App1
17	475	77.4	115	6	US-10-981-300-53 Sequence 53, App1
18	475	77.4	126	6	US-10-994-679-68 Sequence 68, App1
19	473	77.0	120	7	US-11-211-917-108 Sequence 108, App1
20	471.5	76.8	121	7	US-11-211-917-26 Sequence 26, App1
21	471.5	76.8	466	7	US-11-211-917-30 Sequence 30, App1
22	470.5	76.6	119	7	US-11-211-917-18 Sequence 18, App1
23	470.5	76.6	464	7	US-11-211-917-22 Sequence 22, App1
24	469	76.4	108	7	US-11-281-266-82 Sequence 82, App1
25	468.5	76.3	121	6	US-10-994-679-60 Sequence 60, App1

26	465.5	75.8	107	6	US-10-484-105-18 Sequence 18, App1
27	465	75.7	108	7	US-11-281-266-85 Sequence 85, App1
28	464	75.6	244	7	US-11-317-786B-17 Sequence 17, App1
29	464	75.6	448	7	US-11-317-786B-9 Sequence 9, App1
30	462.5	75.3	118	6	US-10-981-300-54 Sequence 54, App1
31	462.5	75.3	443	6	US-10-981-300-20 Sequence 20, App1
32	460.5	75.0	113	7	US-11-290-687-17 Sequence 17, App1
33	460	74.9	247	6	US-10-539-402-10 Sequence 10, App1
34	458.5	74.7	127	7	US-11-259-133-202 Sequence 202, App1
35	458	74.6	244	7	US-11-402-010-77 Sequence 77, App1
36	457	74.4	244	7	US-11-317-786B-19 Sequence 19, App1
37	457	74.4	448	7	US-11-317-786B-11 Sequence 11, App1
38	456	74.3	240	7	US-11-317-786B-15 Sequence 15, App1
39	456	74.3	445	7	US-11-317-786B-32 Sequence 32, App1
40	456	74.3	448	7	US-11-317-786B-7 Sequence 7, App1
41	453	73.8	118	7	US-11-281-266-42 Sequence 42, App1
42	453	73.8	286	7	US-11-154-103-8 Sequence 8, App1
43	451	73.5	112	7	US-11-249-296-64 Sequence 64, App1
44	451	73.5	138	7	US-11-171-085-8 Sequence 8, App1
45	451	73.5	245	6	US-10-539-402-16 Sequence 16, App1

#### ALIGNMENTS

RESULT 1  
US-10-981-300-51  
Sequence 51, Application US//10981300  
Publication No. US20060093599A1  
GENERAL INFORMATION:  
APPLICANT: GIORGIO SENALDI  
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
FILE REFERENCE: ABGX-005  
CURRENT APPLICATION NUMBER: US/10/981,300  
CURRENT FILING DATE: 2004-11-03  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 51  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-981-300-51

Query Match 83.1%; Score 510.5; DB 6; Length 118;  
Best Local Similarity 85.0%; Pred. No. 9,6e-39;  
Matches 96; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 2 ESGRGLVKSQTLSTCTVSGSIRSGYYWVWROPKGLKEMIGNIYHSGNTYVPSL 61  
DB 6 ESGRGLVKSQTLSTCTVSGSIRSGYYWVWROPKGLKEMIGNIYHSGNTYVPSL 65  
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVVSS 114  
DB 66 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVVSS 117

RESULT 2  
US-11-304-986-25  
Sequence 25, Application US//11304986  
Publication No. US20060165682A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth and Neuraltab et al.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA  
FILE REFERENCE: ELN-055  
CURRENT APPLICATION NUMBER: US/11/304,986  
CURRENT FILING DATE: 2005-12-15  
PRIOR APPLICATION NUMBER: 60/636664  
PRIOR FILING DATE: 2004-12-15  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct, consensus sequence for heavy chain  
; OTHER INFORMATION: framework region  
US-11-304-986-25

Query Match 79.6%; Score 488.5; DB 7; Length 119;  
Best Local Similarity 81.9%; Pred. No. 8.8e-37;  
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGYVSWVROPKGLWMIGNIYHSGNTYVPSL 61  
Db 6 ESGPGLVPSQTLSTCTVSGSIRSGYVSWVROPKGLWMIGNIYHSGNTYVPSL 63  
Qy 62 KSRITVSDTSKQNFSLRTSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTVSS 114  
Db 64 KSRVTVSDTSKQNFSLRTSVTAADTAVYYCARWGDDGFYANDYWGQGLTVTVSS 119

RESULT 3  
US-11-355-464-13  
; Sequence 13, Application US/11355464  
; Publication No. US20060147375A1  
; GENERAL INFORMATION:  
; APPLICANT: GUDAS, Jean  
; APPLICANT: JAKOBOVITS, Aya  
; APPLICANT: JIA, Xiao-Chi,  
; APPLICANT: MORRISON, Robert Kendall  
; APPLICANT: CHALILTA-EID, Pia M.  
; APPLICANT: RAITANO, Arthur B.  
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT  
; TITLE OF INVENTION: BIND TO PSCA PROTEINS  
; FILE REFERENCE: 511582008821  
; CURRENT FILING DATE: 2006-02-15  
; PRIOR APPLICATION NUMBER: US/11/355,464  
; PRIOR FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: US 10/857,484  
; PRIOR FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: US 60/672,000  
; PRIOR FILING DATE: 2005-04-14  
; PRIOR APPLICATION NUMBER: US 60/633,077  
; PRIOR FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: US 60/621,310  
; PRIOR FILING DATE: 2004-10-21  
; PRIOR APPLICATION NUMBER: US 60/617,881  
; PRIOR FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: US 60/616,381  
; PRIOR FILING DATE: 2004-10-05  
; PRIOR APPLICATION NUMBER: US 60/475,064  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-355-464-13

Query Match 79.4%; Score 487.5; DB 7; Length 149;  
Best Local Similarity 78.5%; Pred. No. 1.3e-36;  
Matches 95; Conservative 8; Mismatches 9; Indels 9; Gaps 2;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGYVSWVROPKGLWMIGNIYHSGNTYVPSL 61  
Db 4 ESGPGLVPSQTLSTCTVSGSIRSGYVSWVROPKGLWMIGNIYHSGNTYVPSL 63  
Qy 62 KSRITVSDTSKQNFSLRTSVTAADTAVYYCARSDGTYT-----LDNWGQGLTVTVS 113  
Db 64 KSRVTVSDTSKQNFSLRTSVTAADTAVYYCAR-DHITVWGVKGMVDWGQGLTVTVS 122

Qy 114 S 114  
Db 123 S 123

RESULT 4  
US-11-355-464-16  
; Sequence 16, Application US/11355464  
; Publication No. US20060147375A1  
; GENERAL INFORMATION:  
; APPLICANT: GUDAS, Jean  
; APPLICANT: JAKOBOVITS, Aya  
; APPLICANT: JIA, Xiao-Chi,  
; APPLICANT: MORRISON, Robert Kendall  
; APPLICANT: CHALILTA-EID, Pia M.  
; APPLICANT: RAITANO, Arthur B.  
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT  
; TITLE OF INVENTION: BIND TO PSCA PROTEINS  
; FILE REFERENCE: 511582008821  
; CURRENT FILING DATE: 2006-02-15  
; PRIOR APPLICATION NUMBER: US/11/355,464  
; PRIOR FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: US 10/857,484  
; PRIOR FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: US 60/672,000  
; PRIOR FILING DATE: 2005-04-14  
; PRIOR APPLICATION NUMBER: US 60/633,077  
; PRIOR FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: US 60/621,310  
; PRIOR FILING DATE: 2004-10-21  
; PRIOR APPLICATION NUMBER: US 60/617,881  
; PRIOR FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: US 60/616,381  
; PRIOR FILING DATE: 2004-10-05  
; PRIOR APPLICATION NUMBER: US 60/475,064  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-355-464-16

Query Match 79.4%; Score 487.5; DB 7; Length 149;  
Best Local Similarity 78.5%; Pred. No. 1.3e-36;  
Matches 95; Conservative 8; Mismatches 9; Indels 9; Gaps 2;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGYVSWVROPKGLWMIGNIYHSGNTYVPSL 61  
Db 4 ESGPGLVPSQTLSTCTVSGSIRSGYVSWVROPKGLWMIGNIYHSGNTYVPSL 63  
Qy 62 KSRITVSDTSKQNFSLRTSVTAADTAVYYCARSDGTYT-----LDNWGQGLTVTVS 113  
Db 64 KSRVTVSDTSKQNFSLRTSVTAADTAVYYCAR-DHITVWGVKGMVDWGQGLTVTVS 122  
Qy 114 S 114  
Db 123 S 123

RESULT 5  
US-10-981-300-52  
; Sequence 52, Application US/10981300  
; Publication No. US20060093599A1  
; GENERAL INFORMATION:  
; APPLICANT: GIORGIO SENALDI  
; APPLICANT: GAZIT-BORNESTEIN  
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
; FILE REFERENCE: ABGX-005

CURRENT APPLICATION NUMBER: US/10/981,300  
CURRENT FILING DATE: 2004-11-03  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-981-300-52

Query Match 79.1%; Score 485.5; DB 6; Length 118;  
Best Local Similarity 81.4%; Pred. No. 1,6e-36;  
Matches 92; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPGKGLWIGNIYHSGNTYNNPSL 61  
DB 6 QGGPGIVKPSQTLSTLCTVSGDISGGMWMIHQPGKGLWIGIYIYSGSYNNPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVYSS 114  
DB 66 KSRFTISVDTSKNQFSLKLTSTVTAADTAVYYCARTGDY-FDYWGGLTVYSS 117

## RESULT 6

US-10-981-300-4  
Sequence 4, Application US/10981300  
Publication No. US20060093599A1  
GENERAL INFORMATION:  
APPLICANT: GIORGIO SENALDI  
APPLICANT: GADI GAJIT-BORNSTEIN  
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
FILE REFERENCE: ABQY-005  
CURRENT APPLICATION NUMBER: US/10/981,300  
CURRENT FILING DATE: 2004-11-03  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 180  
TYPE: PRT  
ORGANISM: homo sapien  
US-10-981-300-4

Query Match 79.1%; Score 485.5; DB 6; Length 180;  
Best Local Similarity 81.4%; Pred. No. 2.4e-36;  
Matches 92; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPGKGLWIGNIYHSGNTYNNPSL 61  
DB 6 QGGPGIVKPSQTLSTLCTVSGDISGGMWMIHQPGKGLWIGIYIYSGSYNNPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMWGQGLTVYSS 114  
DB 66 KSRFTISVDTSKNQFSLKLTSTVTAADTAVYYCARTGDY-FDYWGGLTVYSS 117

## RESULT 7

US-11-337-300-84  
Sequence 84, Application US/11337300  
Publication No. US20060121580A1  
GENERAL INFORMATION:  
APPLICANT: Crucell Holland B.V.  
APPLICANT: ter Meulen, Jan H.  
APPLICANT: De Kruijf, Cornelis A.  
APPLICANT: van den Brink, Edward N.  
APPLICANT: Goudemil, Jaap  
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
FILE REFERENCE: 0091 WO 00 ORD  
CURRENT APPLICATION NUMBER: US/11/337,300  
CURRENT FILING DATE: 2006-01-20  
NUMBER OF SEQ ID NOS: 478  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 84

LENGTH: 121  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Variable heavy chain of SC03-017  
US-11-337-300-84

Query Match 78.7%; Score 483.5; DB 7; Length 121;  
Best Local Similarity 80.0%; Pred. No. 2.5e-36;  
Matches 92; Conservative 11; Mismatches 9; Indels 3; Gaps 2;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPGKGLWIGNIYHSGNTYNNPSL 61  
DB 8 EGGAGLTKPSFTSLTCTVSGSVSGSYVSWVRQPPGKGLWIGIYIYSGSTNNPSL 67

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA--RSDGYTLDMWGQGLTVYSS 114  
DB 68 KSRVITSDVTSKNQFSLKLTSTVTAADTAVYYCAKRSAGF-FDYWGQGLTVYSS 121

## RESULT 8

US-11-337-300-94  
Sequence 94, Application US/11337300  
Publication No. US20060121580A1  
GENERAL INFORMATION:  
APPLICANT: Crucell Holland B.V.  
APPLICANT: ter Meulen, Jan H.  
APPLICANT: De Kruijf, Cornelis A.  
APPLICANT: van den Brink, Edward N.  
APPLICANT: Goudemil, Jaap  
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
FILE REFERENCE: 0091 WO 00 ORD  
CURRENT APPLICATION NUMBER: US/11/337,300  
CURRENT FILING DATE: 2006-01-20  
NUMBER OF SEQ ID NOS: 478  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 94  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: SC03-017  
US-11-337-300-94

Query Match 78.7%; Score 483.5; DB 7; Length 248;  
Best Local Similarity 80.0%; Pred. No. 5e-36;  
Matches 92; Conservative 11; Mismatches 9; Indels 3; Gaps 2;

QY 2 EGGPGIVKPSQTLSTLCTVSGSIRSGYVSWVRQPPGKGLWIGNIYHSGNTYNNPSL 61  
DB 9 EGGAGLTKPSFTSLTCTVSGSVSGSYVSWVRQPPGKGLWIGIYIYSGSTNNPSL 68

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA--RSDGYTLDMWGQGLTVYSS 114  
DB 69 KSRVITSDVTSKNQFSLKLTSTVTAADTAVYYCAKRSAGF-FDYWGQGLTVYSS 122

## RESULT 9

US-11-211-917-82  
Sequence 82, Application US/11211917  
Publication No. US20060093600A1  
GENERAL INFORMATION:  
APPLICANT: BEIDIAN, VAHE  
APPLICANT: GLADIE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 82  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-211-917-82

Query Match 78.4%; Score 481.5; DB 7; Length 121;  
Best Local Similarity 79.7%; Pred. No. 3.8e-36;  
Matches 94; Conservative 8; Mismatches 9; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIR--GYWVWVIRPPGKLEWIGIYVSGSTNVP 63  
QY 62 KSRITWVDTSKNHFSLRLTSVTADTAADTAAYVYCARSDGYTLD-----NMGGTIVTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTADTAADTAAYVYCARRGLYGDYGFAPWGGTIVTVSS 121

## RESULT 10

US-11-211-917-98  
Sequence 98, Application US/11211917  
Publication No. US20060093600A1

GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 98  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-211-917-98

Query Match 78.4%; Score 481.5; DB 7; Length 121;  
Best Local Similarity 79.7%; Pred. No. 3.8e-36;  
Matches 94; Conservative 7; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIR--GYWVWVIRPPGKLEWIGIYVSGSTNVP 63  
QY 62 KSRITWVDTSKNHFSLRLTSVTADTAADTAAYVYCARSDGYTLD-----NMGGTIVTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTADTAADTAAYVYCARRGLYGDYGFAPWGGTIVTVSS 121

## RESULT 11

US-11-211-917-70  
Sequence 70, Application US/11211917  
Publication No. US20060093600A1

GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 70  
LENGTH: 466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-211-917-70

Query Match 78.4%; Score 481.5; DB 7; Length 466;  
Best Local Similarity 79.7%; Pred. No. 1.4e-35;  
Matches 94; Conservative 7; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVPSL 61  
DB 25 ESGPGLVKPSQTLSTCTVSGGSIR--GYWVWVIRPPGKLEWIGIYVSGSTNVP 82  
QY 62 KSRITWVDTSKNHFSLRLTSVTADTAADTAAYVYCARSDGYTLD-----NMGGTIVTVSS 114  
DB 83 KSRVTISVDTSKNQFSLKLSVTADTAADTAAYVYCARRGLYGDYGFAPWGGTIVTVSS 140

## RESULT 12

US-11-211-917-86  
Sequence 86, Application US/11211917  
Publication No. US20060093600A1

GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 86  
LENGTH: 466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-211-917-86

Query Match 78.4%; Score 481.5; DB 7; Length 466;  
Best Local Similarity 79.7%; Pred. No. 1.4e-35;  
Matches 94; Conservative 8; Mismatches 9; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVPSL 61  
DB 25 ESGPGLVKPSQTLSTCTVSGGSIR--GYWVWVIRPPGKLEWIGIYVSGSTNVP 82  
QY 62 KSRITWVDTSKNHFSLRLTSVTADTAADTAAYVYCARSDGYTLD-----NMGGTIVTVSS 114  
DB 83 KSRVTISVDTSKNQFSLKLSVTADTAADTAAYVYCARRGLYGDYGFAPWGGTIVTVSS 140

## RESULT 13

US-11-211-917-66  
Sequence 66, Application US/11211917  
Publication No. US20060093600A1

GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE



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; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 66
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-66

Query Match      78.1%; Score 479.5; DB 7; Length 121;
Best Local Similarity 79.7%; Pred. No. 5.7e-36;
Matches 94; Conservative 6; Mismatches 11; Indels 7; Gaps 2;
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```
QY 2 ESGPGLVKISQTLSTCTVSGGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKISQTLSTCTVSGGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYTLD----NMGGGTLVTYSS 114
DB 64 KSRVITISVDTSKNQFSLKLSSTVTAADTAAYYCARSDGYTLDYGMFAPMGGTLVTYSS 121
```

```
RESULT 14
US-11-211-917-109
; Sequence 109, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-109
```

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Query Match      77.9%; Score 478; DB 7; Length 118;
Best Local Similarity 80.9%; Pred. No. 7.5e-36;
Matches 93; Conservative 8; Mismatches 10; Indels 4; Gaps 2;
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QY 2 ESGPGLVKISQTLSTCTVSGGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKISQTLSTCTVSGGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYTLD----NMGGGTLVTYSS 114
DB 64 KSRVITISVDTSKNQFSLKLSSTVTAADTAAYYCARSDGYTLDYGMFAPMGGTLVTYSS 118
```

RESULT 15

```
US-11-211-917-142
; Sequence 142, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 142
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-142
```

```
Query Match      77.9%; Score 478; DB 7; Length 118;
Best Local Similarity 81.7%; Pred. No. 7.5e-36;
Matches 94; Conservative 8; Mismatches 9; Indels 4; Gaps 3;
```

```
QY 2 ESGPGLVKISQTLSTCTVSGGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKISQTLSTCTVSGGSIRSGYYWVROPFGKLEWIGNIYHSGNTYNNPSL 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGYTLD----NMGGGTLVTYSS 114
DB 64 KSRVITISVDTSKNQFSLKLSSTVTAADTAAYYCARSDGYTLDYGMFAPMGGTLVTYSS 118
```

Search completed: August 30, 2006, 00:52:02  
Job time : 13.4727 secs

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GenCore version 5.1.9  
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OW protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 102.427 Seconds  
(without alignments)  
508.875 Million cell updates/sec

Title: US-10-027-725a-7  
Perfect score: 609  
Sequence: 1 LBSGFLVKAQTLISCAV.....RLDGYTLIDWGQTLVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	114	5	ABG30445 Human Ige
2	547	89.8	114	5	ABG30447 Human Ige
3	546	89.7	114	5	ABG30446 Human Ige
4	519	85.2	122	7	ADP03977 Murine-ex
5	518.5	85.1	121	7	ADP03982 Murine-ex
6	517.5	85.0	125	7	ADP03871 Murine-ex
7	514.5	84.5	121	7	ADP03981 Murine-ex
8	512	84.1	118	7	ADP03968 Murine-ex
9	512	84.1	120	7	ADP03974 Murine-ex
10	512	84.1	120	7	ADP03873 Murine-ex
11	509.5	83.7	123	7	ADP03872 Murine-ex
12	509.5	83.7	148	10	ABE94855 Antibody
13	509.5	83.7	148	10	ABE94833 Antibody
14	508.5	83.5	123	7	ADP03870 Murine-ex
15	508.5	83.5	123	7	ADP03879 Murine-ex
16	508.5	83.5	123	7	ADP03878 Murine-ex
17	508.5	83.5	125	7	ADP03868 Murine-ex
18	508.5	83.5	125	7	ADP03876 Murine-ex
19	508.5	83.5	144	9	ADX98263 Human ant
20	506.5	83.2	119	7	ADP03961 Murine-ex
21	506.5	83.2	123	2	AAW78433 Antibody
22	506.5	83.2	123	5	ABB97976 Heavy cha
23	506.5	83.2	123	7	ADG88414 anti-Ob-R

24	505.5	83.0	119	7	ADP03970 Murine-ex
25	505	82.9	252	5	ABP45983 Human Bly
26	505	82.9	252	7	ADG96810 Single ch
27	505	82.9	252	9	ADP78863 Human B L
28	504.5	82.8	125	7	ADP03983 Murine-ex
29	504.5	82.8	480	9	ADZ57697 Anti-cMet
30	504	82.8	120	7	ADP03969 Murine-ex
31	503.5	82.7	127	7	ADP03874 Murine-ex
32	503	82.6	124	7	ADP03935 Murine-ex
33	502	82.4	123	4	AB662745 Human HIV
34	501.5	82.3	117	7	ADG99784 Anti-Huma
35	501.5	82.3	117	7	ADP05388 Anti-MUC1
36	501.5	82.3	117	7	ADP09826 Human ant
37	501	82.3	149	9	ADZ57713 Germaline
38	500.5	82.2	123	9	ADX98417 Human ant
39	500.5	82.2	251	6	ABJ19829 Human VEG
40	500.5	82.2	251	8	ADH13871 Human vas
41	500.5	82.2	251	8	AEEO9933 Human VEG
42	500	82.1	125	8	ADSI6556 Human ant
43	499.5	82.0	120	4	AA662775 Human HIV
44	499	81.9	473	4	AA66206 Human imm
45	498.5	81.9	253	5	ABP45608 Human Bly

## ALIGNMENTS

RESULT 1	ABG30445	ABG30445 standard; protein; 114 AA.
XX	XX	XX
AC	ABG30445;	
XX	XX	XX
DT	21-OCT-2002	(first entry)
XX	XX	XX
DE	Human Ige Fab clone 94 heavy chain protein.	
XX	XX	XX
KW	Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;	
XX	XX	XX
OS	timothy grass pollen allergen; passive immunotherapy.	
XX	XX	XX
XX	Homo sapiens.	
XX	XX	XX
FH	Key	Location/Qualifiers
FT	Region	1..26
FT	Region	/note="FR1 region"
FT	Region	27..33
FT	Region	/note="CDR1 region"
FT	Region	34..47
FT	Region	/note="FR2 region"
FT	Region	48..63
FT	Region	/note="CDR2 protein"
FT	Region	64..95
FT	Region	/note="FR3 region"
FT	Region	96..103
FT	Region	/note="CDR2 region"
FT	Region	104..114
FT	Region	/note="FR4 region"
XX	XX	XX
PN	WO200253595-A1.	
XX	XX	XX
XX	11-JUL-2002.	
PD	27-DEC-2001; 2001WO-GB002908.	
XX	XX	XX
PR	29-DEC-2000; 2000SE-00004892.	
XX	XX	XX
PA	(PAA) PHARMACIA DIAGNOSTICS AB.	
XX	XX	XX
PI	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX	XX	XX
DR	WFI, 2002-583604/62.	
DR	N-PSDB; ABR96537.	
XX	XX	XX

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PF      27-DEC-2001; 2001WO-SEQ029308.
PR      29-DEC-2000; 2000SE-00004892.
XX      (PHAA ) PHARMACIA DIAGNOSTICS AB.
PA      Flicker S, Steinberger P, Kraft D, Valenta R;
PI      WPI: 2002-583604/62.
XX      DR N-PSDB; ABRK89639.
XX      Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT      variable region of group 2 allergen specific-human IGE Fabs, useful for
PT      diagnosing or passive immunotherapy of type I allergy, for environmental
PT      allergen detection.
XX      Disclosure; Page 38; 45pp; English.
PS      This invention relates to the DNA and protein sequences of group 2
CC      allergen-specific human IGE Fabs and methods for their use. The proteins
CC      of the invention may have antiallergic activities and may be used as a
CC      vaccine or an inhibitor of binding of grass pollen allergic patient's IGE
CC      antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC      2 allergen-specific fads of the invention may be useful for environmental
CC      allergen detection and for standardisation of allergen extracts. The fads
CC      - or a vaccine against a type I allergy it is also useful for diagnosing a type
CC      I allergy. The allergen-specific fads of the invention are useful for
CC      inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC      also useful for identification of group 2 allergen-containing pollen and
CC      may be used for blocking the binding of grass pollen allergic patients
CC      IGE antibodies to Phi p 2. The present sequence represents the human Ige
CC      fab, clone 100 heavy chain protein of the invention
SQ      Sequence 114 AA:
Query Match          89.8%; Score 547; DB 5; Length 114;
Best Local Similarity    89.5%; Pred. No. 1.8e-42;
Matches 102; Conservative   5; Mismatches   7; Indels   0; Gaps   0;
OY      1 LEEGPGLVKKPACTLSLSCAVSGSIRSGGYWMSWIROHPKGLEMGIVYHSGNTYNPS 60
Db       | |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
        1 LESEGFLVKRPQTSLCTCYTSGGSIRSGGYWMSWIRPPCKGLEMIGNIHSQNTYNPS 60
OY      61 LKSRIAMSVDTSENKFSLRLNSVTADTAAYVCARLDGTLLDWGGTLTVTS 114
Db       | |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
        61 LKSRYTWSVDTSKNHFSLRLSSVTAAOTAVYYCARSDGYTLDMWGQTLTVTS 114
RESULT 3
ABG30446 ID            ABG30446 standard; protein; 114 AA.
XX      AC            ABG30446;
XX      DT            21-OCT-2002 (first entry)
DE      Human IGE Fab clone 60 heavy chain protein.
XX      KM      Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
XX      CS      timothy grass pollen allergen; passive immunotherapy.
OS      Homo sapiens.
XX      Key         Location/Qualifiers
FH      Region      1..26
FT           /note= "FR1 region"
FT           27..33
FT           /note= "CDR1 region"
FT           34..47
FT           /note= "FR2 region"
FT           48..63
FT           /note= "CDR2 protein"
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FT Region 64..95  
 FT /note="PR3 region"  
 FT Region 96..103  
 FT /note="CDR2 region"  
 FT Region 104..114  
 FT /note="PR4 region"  
 XX WO200253595-A1.  
 XX 11-JUL-2002.  
 XX 27-DEC-2001; 2001WO-SE002908.  
 XX 29-DEC-2000; 2000SE-00004892.  
 XX (PHMA) PHARMACIA DIAGNOSTICS AB.  
 XX Flicker S, Steinberger P, Kraft D, Valenta R;  
 XX WPI; 2002-583604/62.  
 XX N-PSDB; ABK89638.  
 XX  
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.  
 XX  
 XX Disclosure; Page 37; 45pp; English.  
 XX  
 XX This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific Fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The Fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific Fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC Fab, clone 60 heavy chain protein of the invention  
 XX  
 XX Sequence 114 AA;  
 SQ  
 Query Match 89.7%; Score 546; DB 5; Length 114;  
 Best Local Similarity 89.5%; Pred. No. 2.3e-42;  
 Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPAQGLTSLSCAVSGSIRSGGYWMSWIRQHPKGLGEMIGIYHSNTYYNPS 60  
 DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRQHPKGLGEMIGIYHSNTYYNPS 60  
 QY 61 LKSRIMSVDTSENKFSRLNSVTAAADTAYYCARLDGYTLIDIMGGGLTVTVSS 114  
 DB 61 LKSRITMSVDTSKNFSRLNSVTAAADTAYYCARLDGYTLIDIMGGGLTVTVSS 114  
 XX  
 XX RESULT 4  
 ADP03977 ID ADP03977 standard; protein; 122 AA.  
 XX  
 XX ADP03977;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.  
 XX  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2003048328-A2.  
 XX 12-JUN-2003.  
 XX 02-DEC-2002; 2002WO-US038550.  
 XX 03-DEC-2001; 2001US-0337275P.  
 XX (ABGE-) ABGENIX INC.  
 XX  
 XX Gudas J, Poltz I, Handa M, Gallo M;  
 XX WPI; 2003-523295/49.  
 XX  
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 XX Example 2; SEQ ID NO 147; 89pp; English.  
 XX  
 XX The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX  
 XX Sequence 122 AA;  
 SQ  
 Query Match 85.2%; Score 519; DB 7; Length 122;  
 Best Local Similarity 81.2%; Pred. No. 7.3e-40;  
 Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;  
 QY 2 ESGPGLVKPAQGLTSLSCAVSGSIRSGGYWMSWIRQHPKGLGEMIGIYHSNTYYNPSL 61  
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWMSWIRQHPKGLGEMIGIYHSNTYYNPSL 65  
 QY 62 KSRIMSVDTSENKFSRLNSVTAAADTAYYCARLDGYTLIDIMGGGLTVTVSS 114  
 DB 66 KSRITMSVDTSKNFSRLNSVTAAADTAYYCARLDGYTLIDIMGGGLTVTVSS 122  
 XX  
 XX RESULT 5  
 ADP03982 ID ADP03982 standard; protein; 121 AA.  
 XX  
 XX ADP03982;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX  
 XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.  
 XX  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX WO2003048328-A2.

```
XX 12-JUN-2003.
PD
XX 02-DEC-2002; 2002MO-US038550.
PF
XX 03-DEC-2001; 2001US-0337275P.
PR
XX (ABGE-) ABGENIX INC.
PA
XX Gudae J, Foltz I, Handa M, Gallo M;
PI
XX WPI; 2003-523295/49.
DR
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 152; 89pp; English.
PS
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 121 AA:
SQ
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Query Match 85.1%; Score 518.5; DB 7; Length 121;
Best Local Similarity 81.9%; Pred. No. 8.1e-40;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;
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QY 2 ESGPGLVKPQOTLSLCAVSGSIRSGYYWSWIRQHPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPQOTLSLCTVSGSISGGYYWSWIRQHPGKGLWIGIYHSGNTYNNPSL 65
QY 62 KSRIRASVDTSENKFSRLNSVTAPADTAVYYCARLD---GYTLDIWGQGLTVTVSS 114
DB 66 KSRVTISVDTSENKQFSLKLSSTVTAADTAVYYCAVYDILTYARDIWGQGMVTVSS 121
```

```
RESULT 6
ADP03871
ID ADP03871 standard; protein; 125 AA.
XX
AC ADP03871;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytostatic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002MO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX
```

```
XX (ABGE-) ABGENIX INC.
PA
XX Gudae J, Foltz I, Handa M, Gallo M;
PI
XX WPI; 2003-523295/49.
DR
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 11; 89pp; English.
PS
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 125 AA:
SQ
```

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Query Match 85.0%; Score 517.5; DB 7; Length 125;
Best Local Similarity 81.7%; Pred. No. 1e-39;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;
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QY 2 ESGPGLVKPQOTLSLCAVSGSIRSGYYWSWIRQHPGKGLWIGIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPQOTLSLCTVSGSISGGYYWSWIRQHPGKGLWIGIYHSGNTYNNPSL 65
QY 62 KSRIRASVDTSENKFSRLNSVTAPADTAVYYCAR----LDGY--TLDIWGQGLTVTVSS 114
DB 66 KSRVTISVDTSENKQFSLKLSSTVTAADTAVYYCARYDYFLTYGPDAFDIWGQGMVTVSS 125
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RESULT 7
ADP03981
ID ADP03981 standard; protein; 121 AA.
XX
AC ADP03981;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 151.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytostatic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002MO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
PA
XX Gudae J, Foltz I, Handa M, Gallo M;
PI
XX WPI; 2003-523295/49.
XX
XX
```

```

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 151; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mab)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 121 AA;
Query Match      84.5%; Score 514.5; DB 7; Length 121;
Best Local Similarity 81.0%; Pred. No. 1.9e-39;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;
OY 2 ESGPGLVPAQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYTHSGNTYNPSTL 61
DB 6 ESGPGLVPAQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYTHSGNTYNPSTL 65
OY 62 KSRIAMSVPTSEKPSLRINSVTAADTAVYYCARL--DGYTLDIMWGQGLVTWSS 114
DB 66 KSRVTTISVDTSKQPSLKLSSTVTAADTAVYYCARVLMFGIGMDVWGQGLVTWSS 121

RESULT 8
ADP03968
ID ADP03968 standard; protein; 118 AA.
XX
AC ADP03968;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytotactic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX MO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J, Foltz J, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 138; 89pp; English.

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XX
XX The invention relates to a novel isolated monoclonal antibody (mab)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
XX
SQ Sequence 118 AA;
Query Match      84.1%; Score 512; DB 7; Length 118;
Best Local Similarity 83.2%; Pred. No. 3.1e-39;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
OY 2 ESGPGLVPAQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYTHSGNTYNPSTL 61
DB 6 ESGPGLVPAQTSLSCAVSGSIRSGGYWMIROHPGKLEWIGYTHSGNTYNPSTL 65
OY 62 KSRIAMSVPTSEKPSLRINSVTAADTAVYYCARLDGYTLDIMWGQGLVTWSS 114
DB 66 KSRVTTISVDTSKQPSLKLSSTVTAADTAVYYCARVYGGSDYWGQGLVTWSS 118

RESULT 9
ADP03974
ID ADP03974 standard; protein; 120 AA.
XX
AC ADP03974;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytotactic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
XX
XX MO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudae J, Foltz J, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 144; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mab)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention

```

CC demonstrates cytoskeletal activity and may be useful for treating a tumour,  
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
CC tumour or breast cancer, possibly via gene therapy. The current sequence  
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
CC (heavy chain variable domain) protein of the invention. The protein was  
CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX SQ Sequence 120 AA;

XX Query Match 84.1%; Score 512; DB 7; Length 120;  
XX Best Local Similarity 81.9%; Pred. No. 3.2e-39;  
XX Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVKPAGQTSLSCAVSGSIRSGYWSWIRQHPKGLGEMIGYIHSGNTYNPSTL 61  
DB 6 ESGPGLVKPAGQTSLSCAVSGSIRSGYWSWIRQHPKGLGEMIGYIHSGNTYNPSTL 65

QY 62 KSRIVSVDTSENKFSRLNSVTAAADTAVYYCARLDGYT---LDIWGGTLYTVSS 114  
DB 66 KSRIVSVDTSENKFSRLNSVTAAADTAVYYCAR-DGNYWYWFDMGRGTLTVSS 120

Db

RESULT 10  
ADP03873 standard; protein; 120 AA.

XX ADP03873;  
XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytoskeletal; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.  
XX MO2003048328-A2.  
XX 12-JUN-2003.  
XX 02-DEC-2002; 2002MO-US038550.  
XX 03-DEC-2001; 2001US-0337275P.  
XX (ABGE-) ABGENIX INC.  
XX Gudaa J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX DR

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 13; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytoskeletal activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a  
CC transgenic mouse strain.

XX SQ Sequence 120 AA;

XX Query Match 84.1%; Score 512; DB 7; Length 120;  
XX Best Local Similarity 81.9%; Pred. No. 3.2e-39;  
XX Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVKPAGQTSLSCAVSGSIRSGYWSWIRQHPKGLGEMIGYIHSGNTYNPSTL 61  
DB 6 ESGPGLVKPAGQTSLSCAVSGSIRSGYWSWIRQHPKGLGEMIGYIHSGNTYNPSTL 65

QY 62 KSRIVSVDTSENKFSRLNSVTAAADTAVYYCARLDGYT---LDIWGGTLYTVSS 114  
DB 66 KSRIVSVDTSENKFSRLNSVTAAADTAVYYCAR-DGNYWYWFDMGRGTLTVSS 120

Db

RESULT 11  
ADP03872 standard; protein; 123 AA.

XX ADP03872;  
XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 12.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
XX cytoskeletal; colorectal neoplasm; renal cell carcinoma;  
XX cervical intraepithelial squamous neoplasia;  
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
XX gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.  
XX MO2003048328-A2.  
XX 12-JUN-2003.  
XX 02-DEC-2002; 2002MO-US038550.  
XX 03-DEC-2001; 2001US-0337275P.  
XX (ABGE-) ABGENIX INC.  
XX Gudaa J, Foltz I, Handa M, Gallo M;  
XX WPI; 2003-523295/49.  
XX DR

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 12; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)  
XX comprising a heavy chain polypeptide and light chain polypeptide having a  
XX sequence chosen from one of 53 fully defined amino acid sequences given  
XX in the specification, where the antibody specifically binds carbonic  
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
XX demonstrates cytoskeletal activity and may be useful for treating a tumour,  
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal  
XX tumour or breast cancer, possibly via gene therapy. The current sequence  
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
XX (heavy chain variable domain) protein of the invention. The protein was  
XX generated via the introduction of the human CA IX protein into a  
XX transgenic mouse strain.

XX SQ Sequence 123 AA;

XX Query Match 83.7%; Score 509.5; DB 7; Length 123;



Best Local Similarity 78.8%; Pred. No. 5.5e-39;  
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;  
QY 2 EGGPGLVKPAQTLISCAVSGSIRSGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 61  
DB 6 EGGPGLVKPSQTLISLCTVSGSSISGGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 65  
QY 62 KSRIVMSVDTSENKPSLRNLSVTADTAVYYCARL-----DGYTLDIWGQGLVTVSS 114  
DB 66 KSRIVTSVDTSENKPSLRNLSVTADTAVYYCARVILMFEDYGVDMVGQGLVTVSS 123  
RESULT 12  
ID AEE94855 standard; protein; 148 AA.  
AC AEE94855;  
XX  
XX  
XX 23-FEB-2006 (first entry)  
DT  
XX  
XX Antibody VH region specific for antigen PSCA, SEQ ID: 35.  
DE  
XX  
XX monoclonal antibody; diagnosis; diagnostic; pharmaceutical;  
KM drug screening; cell proliferation; cancer; cytostatic; neoplasm; tumor;  
KM PSCA; antibody.  
XX  
XX Homo sapiens.  
XX  
XX WO2005118864-A2.  
XX  
XX  
XX 15-DEC-2005.  
PD  
XX  
XX 17-MAY-2005; 2005MO-US017412.  
PF  
XX  
XX 28-MAY-2004; 2004US-00857484.  
PR 28-MAY-2004; 2004MO-US017231.  
PR 05-OCT-2004; 2004US-0616381P.  
PR 12-OCT-2004; 2004US-0617881P.  
PR 21-OCT-2004; 2004US-0621310P.  
PR 02-DEC-2004; 2004US-0633077P.  
PR 14-APR-2005; 2005US-0672000P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Gudae J, Jakobovits A, Jia X, Morrison RK, Morrison KM, Shao H;  
PI Challita-Eid PM, Raitano AB;  
PI  
XX  
XX MPI; 2006-047570/05.  
DR  
XX  
XX N-PSDB; AEE94854.  
XX  
XX  
XX New antibody that binds to PSCA protein, useful for diagnosing,  
PT prognosing, preventing, and/or treating cancer, e.g. prostate, pancreas,  
PT bladder, kidney, colon, lung, ovary, or breast cancer.  
XX  
XX  
XX Disclosure; SEQ ID NO 35; 282zp; English.  
XX  
XX  
XX The new invention relates to antibodies and binding fragments that bind  
CC to PSCA proteins. PSCA, referred to as PSCA v.1 in the specification, was  
CC identified as an antigen expressed in prostate cancer. Specifically given  
CC is an antibody or fragment comprising an antigen-binding site that binds  
CC specifically to PSCA protein. Also given are a transgenic animal that  
CC produces the monoclonal antibody; a hybridoma that produces the  
CC monoclonal antibody; a vector comprising a polynucleotide encoding the  
CC antibody; a pharmaceutical that comprises the antibody or fragment in a  
CC human unit dose form; an assay or a method for detecting the presence of a  
CC PSCA protein; a method of inhibiting growth of cells that express PSCA;  
CC a composition comprising PSCA siRNA (double stranded RNA) that  
CC corresponds to the nucleic acid that encodes a protein; a method for  
CC identifying a molecule that modulates cell proliferation or a therapeutic  
CC for treating a cancer listed in the specification; a method for treating  
CC cancer; and a method for reducing tumor growth. The antibody is a  
CC monoclonal, humanized antibody. The antigen-binding site is a murine  
CC antigen-binding domain. The antibody is coupled to a detectable marker, a

CC toxin, a therapeutic agent, or a chemotherapeutic agent. The antigen-  
CC binding site specifically binds to an epitope within amino acids of a  
CC protein comprising any of 21 sequences (SEQ ID NOS: 13-33). The antibody,  
CC protein, composition, vaccines, and method are useful for diagnosing,  
CC prognosing, preventing, and/or treating cancer. The present sequence is a  
CC VH region of an antibody specific for PSCA protein.  
XX  
SQ Sequence 148 AA;  
Query Match 83.7%; Score 509.5; DB 10; Length 148;  
Best Local Similarity 78.5%; Pred. No. 6.7e-39;  
Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;  
QY 2 EGGPGLVKPAQTLISCAVSGSIRSGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 61  
DB 15 EGGPGLVKPSQTLISLCTVSGSSISGGYWMIRHPGKGLMIGIYIHSGNTYNNPSL 74  
QY 62 KSRIVMSVDTSENKPSLRNLSVTADTAVYYCARLDG-----YTLDIWGQGLVTVSS 113  
DB 75 KSRIVMSVDTSENKPSLRNLSVTADTAVYYCAR-DGITMIRGYGYGMDVGQGLVTVSS 133  
QY 114 S 114  
DB 134 S 134  
RESULT 13  
ID AEE94833 standard; protein; 148 AA.  
AC AEE94833;  
XX  
XX  
XX 23-FEB-2006 (first entry)  
DT  
XX  
XX Antibody VH region specific for cancer antigen PSCA, SEQ ID: 13.  
DE  
XX  
XX monoclonal antibody; diagnosis; diagnostic; pharmaceutical;  
KM drug screening; cell proliferation; cancer; cytostatic; neoplasm; tumor;  
KM PSCA; antibody.  
XX  
XX Homo sapiens.  
XX  
XX WO2005118864-A2.  
XX  
XX  
XX 15-DEC-2005.  
PD  
XX  
XX 17-MAY-2005; 2005MO-US017412.  
PF  
XX  
XX 28-MAY-2004; 2004US-00857484.  
PR 28-MAY-2004; 2004MO-US017231.  
PR 05-OCT-2004; 2004US-0616381P.  
PR 12-OCT-2004; 2004US-0617881P.  
PR 21-OCT-2004; 2004US-0621310P.  
PR 02-DEC-2004; 2004US-0633077P.  
PR 14-APR-2005; 2005US-0672000P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Gudae J, Jakobovits A, Jia X, Morrison RK, Morrison KM, Shao H;  
PI Challita-Eid PM, Raitano AB;  
PI  
XX  
XX MPI; 2006-047570/05.  
DR  
XX  
XX  
XX New antibody that binds to PSCA protein, useful for diagnosing,  
PT prognosing, preventing, and/or treating cancer, e.g. prostate, pancreas,  
PT bladder, kidney, colon, lung, ovary, or breast cancer.  
XX  
XX  
XX Disclosure; SEQ ID NO 13; 282zp; English.  
XX  
XX  
XX The new invention relates to antibodies and binding fragments that bind  
CC to PSCA proteins. PSCA, referred to as PSCA v.1 in the specification, was  
CC identified as an antigen expressed in prostate cancer. Specifically given  
CC is an antibody or fragment comprising an antigen-binding site that binds

CC specifically to PSCA protein. Also given are a transgenic animal that  
 CC produces the monoclonal antibody; a hybridoma that produces the  
 CC monoclonal antibody; a vector comprising a polynucleotide encoding the  
 CC antibody; a pharmaceutical that comprises the antibody or fragment in a  
 CC human unit dose form; an assay or a method for detecting the presence of  
 CC a PSCA protein; a method of inhibiting growth of cells that express PSCA;  
 CC a composition comprising PSCA siRNA (double stranded RNA) that  
 CC corresponds to the nucleic acid that encodes a protein; a method for  
 CC identifying a molecule that modulates cell proliferation or a therapeutic  
 CC for treating a cancer listed in the specification; a method for treating  
 CC cancer; and a method for reducing tumor growth. The antibody is a  
 CC monoclonal, humanized antibody. The antigen-binding site is a murine  
 CC antigen-binding domain. The antibody is coupled to a detectable marker, a  
 CC toxin, a therapeutic agent, or a chemotherapeutic agent. The antigen-  
 CC binding site specifically binds to an epitope within amino acids of a  
 CC protein comprising any of 21 sequences (SEQ ID NOS: 13-33). The antibody,  
 CC protein, composition, vaccines, and method are useful for diagnosing,  
 CC prognosing, preventing, and/or treating cancer. The present sequence is  
 CC an VH region of an antibody specific for PSCA protein.

XX  
 SQ Sequence 148 AA;

Query Match 83.7%; Score 509.5; DB 10; Length 148;  
 Best Local Similarity 78.5%; Pred. No. 6,7e-39;

Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;

QY 2 ESGPGVLVKAQQTLSLCAVSGSGIRSGYVWSWIRQHPKGLWIGIYHSGNTYVPSL 61

DB 15 ESGPGVLVKAQQTLSLCTVSGSGISGGYVWIRQHPKGLWIGIYHSGNTYVPSL 74

QY 62 KSRFMSVDTSEKFSRLNSVTADTAIVYCARLDG-----YTLIDIWGQGLTVTVS 113

DB 75 KSRFMSVDTSEKFSRLNSVTADTAIVYCARLDG-----YTLIDIWGQGLTVTVS 133

QY 114 S 114

DB 134 S 134

RESULT 14

ID ADP03870 standard; protein; 123 AA.

XX ADP03870;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytotaratic; colorectal neoplasm; renal cell carcinoma;

KM cervical intraepithelial squamous neoplasia; oesophageal; breast cancer;

KM gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 10; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytotaratic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, esophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

CC  
 SQ Sequence 123 AA;

Query Match 83.5%; Score 508.5; DB 7; Length 123;  
 Best Local Similarity 80.5%; Pred. No. 6,8e-39;

Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGVLVKAQQTLSLCAVSGSGIRSGYVWSWIRQHPKGLWIGIYHSGNTYVPSL 61

DB 6 ESGPGVLVKAQQTLSLCTVSGSGISGGYVWIRQHPKGLWIGIYHSGNTYVPSL 65

QY 62 KSRFMSVDTSEKFSRLNSVTADTAIVYCARLDG-----YTLIDIWGQGLTVTVS 114

DB 66 KSRFMSVDTSEKFSRLNSVTADTAIVYCARLDG-----YTLIDIWGQGLTVTVS 123

RESULT 15

ID ADP03879 standard; protein; 123 AA.

XX ADP03879;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 19.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytotaratic; colorectal neoplasm; renal cell carcinoma;

KM cervical intraepithelial squamous neoplasia;

KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KM gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 19; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mab)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cyrostatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.

XX  
 SQ Sequence 123 AA;

Query Match 83.5%; Score 508.5; DB 7; Length 123;  
 Best Local Similarity 80.5%; Pred. No. 6.8e-39;  
 Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYTMSWIRHFGKLEWIGYIYHSGNTYNNPSL 61  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 6 ESGPGLVKPESQTLSTCTVSGGSINSGYYTMSWIRHFGKLEWIGYIYSGSTYNNPSL 65  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 62 KSRIAMSVDTSFNKFSIRLNSVTADTAATYTCAR----LDGYTLDIWGQGLVTVSS 114  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 66 KSRVLIISVDTSFNQPSLKLSSVTADTAATYTCARERTDYDYYGLDVMGQGLVTVSS 123  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: August 30, 2006, 00:41:53  
 Job time : 103.427 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 10.7091 Seconds  
(without alignments)  
1024.243 Million cell updates/sec

Title: US-10-027-725A-7

Sequence: 1 LBSGPELVPAQTLSLSCAV.....RLDGYTLDIWGQTLVTSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479.5	78.7	116	2 S37456	Ig mu chain - huma
2	476.5	78.2	135	2 S78051	Ig heavy chain pre
3	475.5	78.1	128	2 S31514	Ig heavy chain - h
4	465	76.4	122	2 S69912	Ig V-D-J region (N
5	464.5	76.3	147	2 S13519	Ig heavy chain V r
6	460	75.5	130	2 S30534	Ig heavy chain V r
7	458.5	75.3	140	2 I37782	Ig variable region
8	453	74.4	99	2 S26801	Ig heavy chain V r
9	452.5	74.3	146	2 S09710	Ig heavy chain V r
10	451.5	74.1	121	2 S44113	Ig heavy chain V r
11	451.5	74.1	130	2 S31690	Ig heavy chain V r
12	450.5	74.0	127	2 S19668	Ig heavy chain V r
13	450.5	74.0	146	2 S09711	Ig heavy chain V r
14	449.5	73.8	155	2 S31511	Ig heavy chain - h
15	446.5	73.3	155	2 S31512	Ig heavy chain - h
16	444	72.9	137	2 S31676	Ig heavy chain V r
17	440	72.2	139	2 S31586	Ig heavy chain V r
18	439	72.1	145	2 S78055	Ig heavy chain pre
19	436	71.6	99	2 S26803	Ig heavy chain V r
20	435.5	71.5	123	2 S30530	Ig heavy chain V r
21	434	71.3	129	2 S44114	Ig heavy chain V r
22	433.5	71.2	117	2 S34964	Ig heavy chain pre
23	432.5	71.0	109	2 PH1673	Ig heavy chain V r
24	431	70.8	99	2 S26802	Ig heavy chain V r
25	430	70.6	97	2 PL0118	Ig heavy chain V-I
26	430	70.6	99	2 S26899	Ig heavy chain V-I
27	427	70.1	110	2 S44110	Ig heavy chain V-D
28	426	70.0	139	2 A41287	Ig heavy chain pre
29	425.5	69.9	121	2 C55257	Ig gamma heavy cha

30	424	69.6	118	2 A26340	Ig heavy chain pre
31	423	69.5	118	2 S20780	Ig heavy chain V r
32	421.5	69.2	140	2 A49045	Ig heavy chain V r
33	419.5	68.9	129	1 D2HUMA	Ig heavy chain V-I
34	419	68.8	135	2 S31604	Ig heavy chain V r
35	418.5	68.7	99	2 A38911	Ig heavy chain V r
36	418	68.6	99	2 S26807	Ig heavy chain V r
37	417	68.5	115	2 S57464	Ig heavy chain V-D
38	417	68.5	126	2 S47010	Ig heavy chain V-D
39	417	68.5	140	2 S78052	Ig heavy chain pre
40	416.5	68.4	140	2 A24770	Ig heavy chain pre
41	415.5	68.2	143	2 B49028	Ig heavy chain V-I
42	415	68.1	99	2 S12418	Ig heavy chain V r
43	414.5	68.1	137	2 S31585	Ig heavy chain V r
44	414	68.0	120	2 PT0370	Ig mu chain precu
45	412.5	67.7	98	2 S26502	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

S37456  
Ig mu chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
R/McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
Submitted to the EMBL Data Library, September 1993  
A/Description: Cloning and analysis of human igm anti-Thyroglobulin autoantibodies from i  
A/Reference number: S37453  
A/Accession: S37456  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-116 <MCI>  
A/Cross-references: UNIPARC:UP100001161C0; EMBL:X75024; NID:G404313; PIDN:CAA52932.1; PII  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
P/6-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 479.5; DB 2; Length 116;  
Best local similarity 76.1%; Pred. No. 76-38;  
Matches 89; Conservative 14; Mismatches 5; Indels 9; Gaps 2;

Qy	6	GLVKAQTSLSCAVGCGSTRSGGYWMSWTRHPRGKLEMGTYHSNNTYVPSLSKSR	65
Db	1	GLVKAQTSLSCAVGCGSTRSGGYWMSWTRHPRGKLEMGTYHSNNTYVPSLSKSR	60
Qy	66	AMSDTSENKFSRLNSVTAAADTAAYVYCARLDGVT-----LDIWGQTLVTSS	114
Db	61	TISVDTSKQFSLKLSVTRADTAAYVYCAR-GGYSYGYVYVMDVWGKTTVTSS	116

##### RESULT 2

S78051  
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C/Accession: S78051; S23716  
R/Haridranath, N.  
Submitted to the EMBL Data Library, August 1990  
A/Reference number: S78051  
A/Accession: S78051  
A/Molecule type: mRNA  
A/Residues: 1-135 <HAR>  
A/Cross-references: UNIPARC:UP10000115B87; EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID  
Int. Immunol. 3, 865-875, 1991  
A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A/Reference number: S23716; MUID:92031262; PMID:1718404  
A/Accession: S23716  
A/Molecule type: mRNA

A:Residues: 13-111 <HAM>  
 A:Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>  
 F:27-111/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 476.5; DB 2; Length 135;  
 Best Local Similarity 76.3%; Pred. No. 1.6e-37;  
 Matches 90; Conservative 13; Mismatches 10; Indels 5; Gaps 2;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGYYSWIRHPGKGLWIGIYHSGNTYNPSTL 61  
 DB 18 ESGPGLVKSFTSLTCTVSGSISGSHYWGIRPPGKGLWISGTYNPSTL 77  
 QY 62 KSRIMSVDTSENKFSRLNSVTADTAVYYCARL--DGYTL--DIWGQGLTVTVSS 114  
 DB 78 KSRVITSDTSKNQFSKLKLSVTADTAVYYCARLGPDDYTLDDGMVWGQGLTVTVSS 135

RESULT 3  
 S31514  
 Ig heavy chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C/Accession: S31514  
 R:Chaetagne, P.; Demaison, C.; Theze, J.; Zouali, M.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
 A:Reference number: S31509  
 A:Accession: S31514  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-128 <CHA>  
 A:Cross-references: UNIPARC:UPI0001160PB; EMBL:X69862; NID:G33086; PIDN:CAA49496.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:22-106/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 475.5; DB 2; Length 128;  
 Best Local Similarity 76.7%; Pred. No. 1.9e-37;  
 Matches 89; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGYYSWIRHPGKGLWIGIYHSGNTYNPSTL 61  
 DB 13 ESGPGLVKSFTSLTCTVSGSISGSHYWGIRHPGKGLWISGTYNPSTL 72  
 QY 62 KSRIMSVDTSENKFSRLNSVTADTAVYYCARL--DGYTL--DIWGQGLTVTVSS 114  
 DB 73 KSRVITSDTSKNQFSRLKLSVTADTAVYYCARLIGYNGFDPGKGLTVTVSS 128

RESULT 4  
 S69912  
 Ig V-D-J region (ND) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C/Accession: S69912  
 R:Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.  
 Leukemia 8, 1285-1289, 1994  
 A>Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi  
 A:Reference number: S69909; MUID:94353315; PMID:8057663  
 A:Accession: S69912  
 A>Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-122 <SAH>  
 A:Cross-references: UNIPARC:UPI0000116640; EMBL:Z33398; NID:G871347; PIDN:CAA83849.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 465; DB 2; Length 122;

Best Local Similarity 75.2%; Pred. No. 1.7e-36;  
 Matches 88; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGYYSWIRHPGKGLWIGIYHSGNTYNPSTL 61  
 DB 6 ESGPGLVKSFTSLTCTVSGSISGSHYWGIRPPGKGLWISGTYNPSTL 65  
 QY 62 KSRIMSVDTSENKFSRLNSVTADTAVYYCARL--LDGYTL--DIWGQGLTVTVSS 114  
 DB 66 KSRVITSDTSKNQFSKLKLSVTADTAVYYCARLGPDDYTLDDGMVWGQGLTVTVSS 122

RESULT 5  
 S13519  
 Ig heavy chain V region precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S13519  
 R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
 Nucleic Acids Res. 19, 673, 1991  
 A>Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
 A:Reference number: S13519; MUID:91187691; PMID:2011536  
 A:Accession: S13519  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-147 <MOR>  
 A:Cross-references: UNIPARC:UPI000115B85; EMBL:X56158; NID:G37724; PIDN:CAA39626.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 464.5; DB 2; Length 147;  
 Best Local Similarity 75.9%; Pred. No. 2.3e-36;  
 Matches 88; Conservative 11; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGYYSWIRHPGKGLWIGIYHSGNTYNPSTL 61  
 DB 32 ESGPGLVKSFTSLTCTVSGSISGSHYWGIRPPGKGLWISGTYNPSTL 91  
 QY 62 KSRIMSVDTSENKFSRLNSVTADTAVYYCARL--LDGYTL--DIWGQGLTVTVSS 114  
 DB 92 KSRVITSDTSKNQFSKLKLSVTADTAVYYCARLPLMGELFDYWGQGLTVTVSS 147

RESULT 6  
 S30534  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
 C/Accession: S30534  
 R:Marlette, X.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S30520  
 A:Accession: S30534  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <MAR>  
 A:Cross-references: UNIPARC:UPI0000113F45; EMBL:Z18320  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 460; DB 2; Length 130;  
 Best Local Similarity 72.8%; Pred. No. 5.3e-36;  
 Matches 91; Conservative 10; Mismatches 12; Indels 12; Gaps 2;

QY 2 ESGPGLVKAQTLISCAVSGSIRSGYYSWIRHPGKGLWIGIYHSGNTYNPSTL 61  
 DB 6 ESGPGLVKSFTSLTCTVSGSISGSHYWGIRPPGKGLWISGTYNPSTL 65  
 QY 62 KSRIMSVDTSENKFSRLNSVTADTAVYYCARL--DGYTL--DIWGQGLTVTVSS 109  
 DB 66 KSRVITSDTSKNQFSKLKLSVTADTAVYYCARLGPDDYTLDDGMVWGQGLTVTVSS 125



## RESULT 11

S31690  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31690  
R/Guisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31690  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-130 <CUI>  
A/Cross-references: UNIPARC:UPI0000116471; EMBL:Z14199; NID:930984; PIDN:CAA78568.1; PID  
A/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/20-102/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 130;  
Best Local Similarity 72.1%; Pred. No. 3.3e-35;  
Matches 88; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 2 ESGPGLVKAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNNPSL 61  
Db 11 ESGPGLVKPSETSLTCTVSGGSISS--YYWSMRQPPGKLEWIGYIYHSGNTYNNPSL 68  
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112  
Db 69 KSRVTVSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 128

QY 113 SS 114  
Db 129 SS 130

## RESULT 12

S19668  
Ig heavy chain V region (VH4DJH6) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 20-Jun-2000  
C/Accession: S19668; S24445  
R/Markes, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A/Title: B7-passing immunization. Human antibodies from V-gene libraries displayed on ph  
A/Reference number: S19663; MUID:92085276; PMID:1748994  
A/Accession: S19668  
A/Molecule type: mRNA  
A/Residues: 1-127 <MAR>  
A/Cross-references: UNIPARC:UPI0000176C7F; EMBL:X61648  
R/Jones, P.T.  
submitted to the EMBL Data Library, October 1991  
A/Reference number: S24442  
A/Accession: S24445  
A/Molecule type: mRNA  
A/Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F' <CON>  
A/Cross-references: UNIPARC:UPI0000115FE7; EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 127;  
Best Local Similarity 69.7%; Pred. No. 3.9e-35;  
Matches 85; Conservative 15; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVKAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNNPSL 61  
Db 6 QSGGGLVKAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNNPSL 65  
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112  
Db 66 KSRVTVSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 125

QY 113 SS 114  
Db 126 SS 127

## RESULT 13

S09711  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S09711  
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A/Reference number: S09710; MUID:9026255; PMID:2111699  
A/Accession: S09711  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-146 <HUG>  
A/Cross-references: UNIPARC:UPI0000176CD3  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 146;  
Best Local Similarity 68.0%; Pred. No. 4.6e-35;  
Matches 83; Conservative 17; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVKAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNNPSL 61  
Db 25 ESGPGLVKPSETSLTCTVSGGSISS--YYWSMRQPPGKLEWIGYIYHSGNTYNNPSL 84  
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112  
Db 85 KSRVTVSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 144

QY 113 SS 114  
Db 145 SS 146

## RESULT 14

S31511  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31511  
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto  
A/Reference number: S31509  
A/Accession: S31511  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-155 <CHA>  
A/Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 449.5; DB 2; Length 155;  
Best Local Similarity 70.8%; Pred. No. 6.1e-35;  
Matches 85; Conservative 15; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGPGLVKAQTLSLSCAVSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYNNPSL 61  
Db 38 ESGPGLVKPSETSLTCTVSGGSISS--YYWSMRQPPGKLEWIGYIYHSGNTYNNPSL 95  
QY 62 KSRIVMSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 114  
Db 96 KSRVTVSVPTSEKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 155



## RESULT 15

S31512

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S31512

R:Chaastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509

A:Accession: S31512

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 &lt;CHA&gt;

A:Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:933082; PIDN:CAA49494.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 73.3%; Score 446.5; DB 2; Length 155;

Best Local Similarity 70.0%; Pred. No. 1,2e-34;

Matches 84; Conservative 16; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWSWIRQPKGLEWIGYIYHSGNTYYNPSTL 61

DB 38 ESGPGLVKPSETLSLCTVSGGSISS--YWSWIRQPKGLEWIGYIYTGSAATYNPPI 95

QY 62 KSRIMSVDTSENKPSRLNSVTADTAAYYCARLDG-----YTIIDTWGQTLVTYSS 114

DB 96 KSRVTISVDTSKNQFSLKSSVTADTAAYYCARGGGSISSWYVYGGMDVWGQGITVTYSS 155

Search completed: August 30, 2006, 00:42:55

Job time : 10.7091 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 62.1818 Seconds  
(without alignments)  
1695.862 Million cell updates/sec

Title: US-10-027-725A-7  
Perfect score: 609  
Sequence: 1 LESGPGLVPAQTLISLSCAV.....RLDGYTLIDMGQTLVTYSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483.5	79.4	476	2	Q6GMX1_HUMAN
2	473	77.7	478	2	Q72379_HUMAN
3	451	74.1	150	2	Q95973_HUMAN
4	449	73.7	477	2	Q6GMX7_HUMAN
5	446.5	73.3	119	2	Q9UL73_HUMAN
6	444	72.9	465	2	Q6GMX6_HUMAN
7	440	72.2	576	2	Q6P418_HUMAN
8	432	70.9	496	2	Q96KX8_HUMAN
9	430.5	70.7	492	2	Q72374_HUMAN
10	430	70.6	620	2	Q96EY0_HUMAN
11	419.5	68.9	129	1	HV2E_HUMAN
12	412.5	67.7	478	2	Q6NTH3_HUMAN
13	409.5	67.2	595	2	Q8WUX4_HUMAN
14	409.5	67.2	597	2	Q6GMX5_HUMAN
15	409.5	67.2	597	2	Q9BUI0_HUMAN
16	409.5	67.2	625	2	Q96A46_HUMAN
17	408	67.0	139	2	Q86SX2_HUMAN
18	405.5	66.6	597	2	Q9BQB8_HUMAN
19	405	66.5	130	2	Q81ZD7_HUMAN
20	405	66.5	146	1	HV2I_HUMAN
21	389	63.9	483	2	Q5U4L3_MOUSE
22	388	63.7	473	2	Q8TC63_HUMAN
23	383	62.9	136	2	Q6LBO5_MOUSE
24	378.5	62.2	615	2	Q659B6_RAT
25	377.5	62.0	479	2	Q9NM22_MOUSE
26	374.5	61.5	137	1	HV46_MOUSE
27	374	61.4	116	2	Q723Y6_HUMAN
28	372.5	61.2	119	2	Q53VR3_HUMAN
29	370.5	60.8	115	2	Q53VQ1_MOUSE
30	370.5	60.8	262	2	Q65Z11_MOUSE
31	369.5	60.7	117	1	HV2G_HUMAN

32	366.5	60.2	590	2	Q569B8_RAT	Q569B8_rattus norv
33	364.5	59.9	119	2	Q53VQ5_MOUSE	Q53VQ5_mus musc
34	362	59.4	120	2	Q53VR7_MOUSE	Q53VR7_mus muscu
35	362	59.4	122	2	Q9UL75_HUMAN	Q9UL75_homo sapien
36	361.5	59.4	113	1	HV47_MOUSE	P01823_mus musc
37	357.5	58.7	476	2	Q6MZX7_HUMAN	Q6MZX7_homo sapien
38	353.5	58.0	119	2	Q53VQ9_MOUSE	Q53VQ9_mus muscu
39	352.5	57.9	98	2	Q53VR2_MOUSE	Q53VR2_mus muscu
40	349.5	57.4	477	2	Q510J1_RAT	Q510J1_rattus norv
41	342.5	56.2	116	1	HV61_MOUSE	P18532_mus muscu
42	341.5	56.1	116	1	HV60_MOUSE	P18531_mus muscu
43	338.5	55.6	98	2	Q53VQ4_MOUSE	Q53VQ4_mus muscu
44	334.5	54.9	98	2	Q53VQ8_MOUSE	Q53VQ8_mus muscu
45	334	54.8	117	1	HV62_MOUSE	P18533_mus muscu

## ALIGNMENTS

RESULT 1  
Q6GMX1\_HUMAN PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1, 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splicein;  
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A.A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splicein;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC Copyrighted by the UniProt Consortium; see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NonDerivs license  
CC EMBL; BC073773; AAH73773.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07654; CL-set; 3.

DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 KW SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 79.4%; Score 483.5; DB 2; Length 476;

Best Local Similarity 72.6%; Pred. No. 7.1e-42;  
 Matches 90; Conservative 16; Mismatches 5; Indels 13; Gaps 2;

QY 2 ESGPGLVKPAQTSLSCAVSGGSIRSGGYWSMIRQHPGKLEWIGYIHSGNTYVNSL 61  
 DB 25 ESGPGLVKPSQTSLTCTVSGGSISGSDYWSMIRQHPGKLEWIGYIHSGNTYVNSL 84  
 QY 62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCAR-----LDGYTLDIWGQTLV 110  
 DB 85 KSRVTSISLDTSKQPSLRKNSVTADTAVYFCARAGVGSFRSWALDGF--NIVGQGTWV 142  
 QY 111 TVSS 114  
 DB 143 TVSS 146

## RESULT 2

072379\_HUMAN

ID 072379\_HUMAN PRELIMINARY; PRT; 478 AA.

AC 072379; 01-OCT-2003, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2003, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Hypothetical protein DKFZp686K04218 (Fragment).

GN Name=DKFZp686K04218;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Human rectum tumor;

RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amid C., Osanger A.,

Pobo G., Han M., Wiemann S.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BX538066; CAD97996.1; -; mRNA.

DR HSSP; P01820; 1G7J.

DR SMR; 072379; 248-456.

DR Ensembl; ENSG00000130076; Homo sapiens.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG\_c1.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR InterPro; IPR013106; V-set.

DR Pfam; PF07654; C1-set; 2.

DR SMART; SM00409; IG; 1.

DR SMART; SM00407; IG; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

DR Hypothetical protein; Immunoglobulin domain; Repeat.

FT NON TER 1

SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 77.7%; Score 473; DB 2; Length 478;  
 Best Local Similarity 75.7%; Pred. No. 9e-41;  
 Matches 87; Conservative 17; Mismatches 2; Gaps 1;

QY 2 ESGPGLVKPAQTSLSCAVSGGSIRSGGYWSMIRQHPGKLEWIGYIHSGNTYVNSL 61  
 DB 24 ESGPGLVKPSQTSLTCTVSGGSISGSDYWSMIRQHPGKLEWIGYIHSGNTYVNSL 83  
 QY 62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARLDGY--TLDIWGQTLVYSS 114  
 DB 84 KSRVTSISLDTSKQPSLRKNSVTADTAVYFCARAGVGSFRSWALDGF--NIVGQGTWV 138

## RESULT 3

095973\_HUMAN

ID 095973\_HUMAN PRELIMINARY; PRT; 150 AA.

AC 095973;

DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1999, sequence version 1.

DT 07-FEB-2006, entry version 23.

DE VHA heavy chain variable region precursor (Fragment).

GN Name=IGM;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;

RT "Clonal proliferation of IGM secreting B cell in the synovium of

RT Behcet's patient with arthritis.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=92031262; PubMed=1718404;

RA Haridraharan N., Goldfarb I.S., Ikematsu H., Burastero S.E.;

RA Wilder R.L., Notkins A.L., Casali P.;

RT "Complete sequence of the genes encoding the VH and VL regions of low-

RT and high-affinity monoclonal IGM and IgM1 rheumatoid factors produced

RT by CD5+ B cells from a rheumatoid arthritis patient.";

RL Int. Immunol. 3:865-875(1991).

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DR EMBL; AF03795; AAC79084.1; -; mRNA.

DR PIR; S31673; S31673.

DR PIR; S78056; S78056.

DR HSSP; P01820; 1G7J.

DR SMR; 095973; 20-147.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG\_v.

DR InterPro; IPR013106; V-set.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin domain; Signal.

FT SIGNAL 1 19

FT CHAIN 20 >150

FT NON TER 150

SEQUENCE 150 AA; 16315 MW; 85664E04938AAAC9 CRC64;

Query Match 74.1%; Score 451; DB 2; Length 150;  
 Best Local Similarity 74.3%; Pred. No. 5e-39;  
 Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 2 ESGPGLVKPAQTSLSCAVSGGSIRSGGYWSMIRQHPGKLEWIGYIHSGNTYVNSL 61  
 DB 25 ESGPGLVKPSQTSLTCTVSGGSISGSDYWSMIRQHPGKLEWIGYIHSGNTYVNSL 84

QY 62 KSRIVMSVDTSENKFSRLNSVTADTAVYYCARLDGYTLDIWGQTLVYSS 114  
 DB 85 KSRVTSISLDTSKQPSLRKNSVTADTAVYFCARAGVGSFRSWALDGF--NIVGQGTWV 137

RESULT 4  
 O6GMX7\_HUMAN PRELIMINARY; PRT; 477 AA.  
 ID O6GMX7\_HUMAN  
 AC O6GMX7  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 16.  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN Nucleotide sequence.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schumacher J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein U.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN Nucleotide sequence.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC  
 CC EMBL: BC073765; AAT73765.1; -; mRNA.  
 DR SRR: O6GMX7; 247-455.  
 DR Ensembl: ENSG00000130076; Homo sapiens.  
 DR InterPro: IPR003599; Ig  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003096; Ig V.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07654; Cl-set; 2.  
 DR SMART: SM00409; IG\_1.  
 DR SMART: SM00407; IG1; 2.  
 DR SMART: SM00406; IG1; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KM Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FES9C09C50CF85 CRC64;  
 SO  
 Query Match 73.7%; Score 449; DB 2; Length 477;  
 Best Local Similarity 75.7%; Pred. No. 3e-38;  
 Matches 87; Conservative 10; Mismatches 14; Indels 4; Gaps 2;  
 QY 2 ESGPGLVKAQTSLSCAVSGGSIIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 61  
 DB 25 EESGGLVKEPSETSLCTVSGGSIIS--YYMSWIRQPGKLEWIGIYHSGNTYNPSTL 82  
 QY 62 KSRIVMSVDTSENKFSRLNLSVTAADTAVYYCARLDG--YTLDIWGGTLVTVSS 114

DB 83 KSRVTLSDTSSKNQFSLRLNSVTAADTAVYYCAHSGSWDFAPFYWGQGLTVTVSS 137  
 RESULT 5  
 Q9UL73\_HUMAN PRELIMINARY; PRT; 119 AA.  
 ID Q9UL73\_HUMAN  
 AC Q9UL73  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 23.  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN Nucleotide sequence.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;  
 RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RN Nucleotide sequence.  
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;  
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,  
 RA Diamond B.,  
 RT "Molecular characteristics of antibodies bearing an anti-DNA-  
 associated idiotype.";  
 RL J. Exp. Med. 174:1639-1652(1991).  
 RN Nucleotide sequence.  
 RX MEDLINE=90059975; PubMed=2511001;  
 RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.,  
 RT "The smaller human VH gene families display remarkably little  
 polymorphism.";  
 RL EMBO J. 8:3741-3748(1989).  
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 CC  
 CC EMBL: AF035041; AAD56277.1; -; mRNA.  
 DR PTR: PH0876; PH0876.  
 DR PTR: S12416; S12416.  
 DR HSSP: P01820; 1G7J.  
 DR SRR: Q9UL73; 2-119.  
 DR Linkhub: Q9UL73; -.  
 DR InterPro: IPR003599; Ig  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig V.  
 DR InterPro: IPR013106; V-set.  
 DR SMART: SM00409; IG\_1.  
 DR SMART: SM00406; IG1; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin domain.  
 FT NON\_TER 1  
 FT NON\_TER 119  
 SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;  
 SO  
 Query Match 73.3%; Score 446.5; DB 2; Length 119;  
 Best Local Similarity 74.1%; Pred. No. 1.e-38;  
 Matches 86; Conservative 12; Mismatches 13; Indels 5; Gaps 2;  
 QY 2 ESGPGLVKAQTSLSCAVSGGSIIRSGGYWMIROHPGKLEWIGIYHSGNTYNPSTL 61  
 DB 6 EESGGLVKEPSETSLCTVSGGSIIS--YYMSWIRQPGKLEWIGIYHSGNTYNPSTL 63  
 QY 62 KSRIVMSVDTSENKFSRLNLSVTAADTAVYYCARLDG--YTLDIWGGTLVTVSS 114  
 DB 64 KSRVTLSDTSSKNQFSLRLNLSVTAADTAVYYCARLDG--YTLDIWGGTLVTVSS 119

RESULT 6

06GMX6\_HUMAN

ID 06GMX6\_HUMAN PRELIMINARY; PRT; 465 AA.

AC 06GMX6;

DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 19-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Aeschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Chisler L., Murnane K., Farmer A.A., Rubin G.M., Hong L., Stopleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Frange C., Rata S.S., Loughellano N.A., Peters G.J., Adamson R.D., Mullaly S.J., Bosnak S.A., McKeown P.J., McKernan K.J., Malek J.A., Gundaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Kirzysinski M.I., Skalska U., Smalusz D.E., Schermer A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Primary B-Cells;

RC Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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CC CC

DR EMBL; BC073766; AAH73766.1; -, mRNA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR InterPro; IPR013106; V-set.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG1.1.

DR SMART; SM00407; IGcl.2.

DR SMART; SM00406; IGV.1.

DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

DR Hypothetical protein.

KW SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

SO

Query Match 72.9%; Score 444; DB 2; Length 465;

Best Local Similarity 77.0%; Pred. No. 9, 6e-38;

Matches 87; Conservative 9; Mismatches 15; Indels 2; Gaps 1;

QY 2 ESGPGLVPAQTLISCAVSGSISGCVYMWIRQHGKGLIEWIGLYHSQNTYVPSL 61

DB 25 ESGPGLVPAQTLISCAVSGSISGCVYMWIRQHGKGLIEWIGLYHSQNTYVPSL 82

62 KSRIAMSVDTSENKFSRLNLSVTAADTVYICARLDGTYTLIDIGWGCTLVYWS 114

**Db**

|||||  
83 KSRVMTSVSDTSSKQFSLKLSSVTIADTAIVYICARGRTTYFDWGCGILTVISS 135  
|||||

**RESULT 7**

O6P418 HUMAN PRELIMINARY; PRI; 576 AA.

AC O6P418; ID Q6P419; CD O6P419; DT 05-JUL-2004, integrated into UniProtKB/TREMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 21-FEB-2006, entry version 20.  
DE IGHG protein.  
GN Name:IGHD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OX Homo.  
NX NCBI\_TaxID=9606;

[1]

RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Feingold E.A., Grosse L.H., Derge J.G.,  
RA Strausberg R.L., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Alechuni S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marutina K., Farmer A.A., Rubin G.W., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P.J., Prange C.,  
RA Brownstein M.J., Udell T.B., Toshimiyuki S., Caminici P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey U., Helton E., Ketteman W., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,  
RA Schmerer A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RA Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

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DR EMBL, BC063384; AAAH63384.1 - mRNA.  
DR HSSP, P01820; IATN.  
DR Ensembl, ENSGEN00000196122; Homo sapiens.  
DR InterPro, IPR0003599; IG.  
DR InterPro, IPR007110; IG-like.  
DR InterPro, IPR0003597; IG cl.  
DR InterPro, IPR003806; IG\_MHC.  
DR InterPro, IPR003596; IG\_V.  
DR InterPro, IPR013151; Immunoglobulin.  
DR InterPro, IPR013106; V-set.  
DR Pfam, PF07654; Cl-set; 1.  
DR SMART, SM00409; IG\_1.  
DR SMART, SM00407; IGcl\_3.  
DR SMART, SM00406; IGV\_1.  
DR PROSITE, PS50835; IG LIKE; 4.  
DR PROSITE, PS00290; IG MHC; UNKNOWN 2.  
SQ SEQUENCE 576 AA; 63364 MW; FEBB97C949D720FILE CRC64;

Query Match 72.2%; Score 440; DB 2; Length 576;  
Best Local Similarity 73.3%; Pred. No. 3.2e-37;  
Matches 85; Conservative 13; Mismatches 14; Indels 4; Gaps 2

Qy 2 ESQGLVAKPQNTLLSICAVSGGSIKSGYQWMSIRHPQKGLFMGIYIHSNGTYNPSTL 6  
Db 32 ESQGLVAKPQNTLLSICAVSGGSIKSGYQWMSIRHPQKGLFMGIYIHSNGTYNPSTL 900  
Qy 62 KSRIAMSVDPSESEKFSILRLSVTAADPAVYVCARLDG---YTLIDWGGGLTVVSS 114  
Db 91 KSRIATISVDSKQNFSLKLSSTVTAADPAVYVCASLDGIYYGMDVWGQGTIVVSS 146

RESULT 8  
Q96KX8 HUMAN PRELIMINARY; PRT; 496 AA.  
AC 096KX8  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 25.  
DE MG27165 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP NCBI EOTIDE SEQUENCE.  
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX STRAUBERG R.L., Feingold E.A., Grose L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,  
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carantini P., Prange C.,  
RA Rana S.S., Loguallano N.A., Peters G.U., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Keltman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalka U., Smellus D.E.,  
RA Schnerf A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NCBI EOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RA Strauberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

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CC -----  
DR EMBL: BC018639; AAH16369.1; -; mRNA.  
DR HSP: BC01876; IOM0.  
DR SMR; Q96KX8; 266-474.  
DR Ensemble; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00407; IGC1; 2.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
DR SEQUENCE 496 AA; 53592 MW; D34652964904069 CRC64;

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Query March 70.9%; Score 432; DB 2; Length 496;
Best Local Similarity 69.2%; Pred. No. 1.9e-36;
Matches 83; Conservative 13; Mismatches 16; Indels 8; Gaps 2;

Qy 2 ESGGGLVKAQAOTLSLCAVSGGSIKSGGYWMIROHPGKLEWIGYIYHSGNTYNSL 61
Db 25 ESGGGLVKAQSETLSLCTCTVSGGSISSSSYWGMIROHPGKLEWIAWTYYSIGITVYNSL 84

Qy 62 KSRIVMSVDTSENKFSRLNSVTAADTAAYVYCARLDGT-----LDINQGLTVYSS 114
Db 85 KSRVTLTSDTSSKNOLSLKRVSVTAADTAAYVFCAR-HGYSRSRGRTGALDYGQGLTVYSS 143

RESULT 9
Q72374_HUMAN PRELIMINARY; PRT; 492 AA.
AC 072374;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Hypothetical protein DKFZp686C02218 (Fragment).
DE Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fodo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BX538077; CAD98001.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q72374; 262-470.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
FT NOX TRR 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760FCA7AB CRC64;

Query Match 70.7%; Score 430.5; DB 2; Length 492;
Best Local Similarity 71.6%; Pred. No. 2.7e-36;
Matches 83; Conservative 13; Mismatches 17; Indels 3; Gaps 2;

Qy 2 ESGGGLVKAQAOTLSLCAVSGGSIKSGGYWMIROHPGKLEWIGYIYHSGNTYNSL 61
Db 37 ESGGGLVKAQSETLSLCTCTVSGGSISSSSYWGMIROHPGKLEWIAWTYYSIGITVYNSL 96

Qy 62 KSRIVMSVDTSENKFSRLNSVTAADTAAYVYCAR-LDG--YTLIDMGQGLTVYSS 114
Db 97 KSRVTLTVDVDSKNFSLRLNSVTAADTAAYVYCAVHVEGPYGMFDPMGQGLTVYSS 152

RESULT 10
Q06EYO_HUMAN PRELIMINARY; PRT; 620 AA.
AC Q06EYO;

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DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 2.  
DT 07-FEB-2006, entry version 26.  
DE IGHM protein.  
GN IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
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RA Stagleon M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
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RA Bonak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunnatone P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Mazy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzyzinski M.T., Skalska U., Smallus D.E.,  
RA Scheraga A., Schein J.E., Jones S.J.W., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91252286; PubMed=1904154;  
RA Neale G.A., Kitchingman G.R.,  
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
RT chain enhancer region contain a 5'-non-translatable exon and are  
RT extremely heterogeneous at the 5' end.";  
RL Nucleic Acids Res. 19:2427-2433 (1991).  
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CC -----  
CC EMBL: BC011857; AAH11857.2; -; mRNA.  
DR PIR: S15590; S15590.  
DR HSDP: P01820; I67J.  
DR SKR: Q96EY0; 27-251.  
DR Ensemble: ENSG00000130076; Homo sapiens.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG\_c1.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR InterPro: IPR013106; V-set.  
DR Pfam: PF07654; C1-set; 4.  
DR SMART: SM00409; IG; 1.  
DR SMART: SM00407; IGc1.3.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG\_LIKE; 5.  
DR PROSITE: PS00290; IG\_MHC; UNKOWN 3.  
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A68FF27B CRC64;

QY	2	ESGGLVLPKPAQTLISLCAVSGGSI	RSGGYYSWIRQHPGKLEWIGIYIHSGNTYTPNSL	61
Db	32	ESGGLVLPKPESTLSTCTVVGSGS	ISS--YVMSWIRCPAGKGLEWIGRIYISGNTYNSPL	89
QY	62	KSRIAMVDPISSENKFSRLNSVTP	ADPAVYYCA----RLGGYTLIDIGGGGLTVVSS	114
Db	90	KSRIYMSVDPISKQFSLKSSVTP	ADPAVYYCASQPMELPTVGLPTVGGGLTVVSS	146
RESULT 11				
ID	HVZF HUMAN	STANDARD;	PRT; 129 AA.	
AC	P01824;			
DT	21-JUL-1986,	integrated into UniProtKB/Swiss-Prot.		
DT	21-JUL-1986,	sequence version 1.		
DE	07-MAR-2006,	entry version 36.		
DE	Ig heavy chain V-II region	MAH.		
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniota;	Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires;	Primates; Catarrhini; Homnidae;		
OC	Homo.			
OX	NCBI_TaxID=9606;			
FN	[1]			
RP	PROTEIN SEQUENCE.			
FX	MEDLINE=82222235; PubMed=6806618;			
RA	Takahashi N., Teneant D., Debuzile B., Lin L.-C., Putnam F.W.;			
RT	"Complete amino acid sequence of the delta heavy chain of human			
RT	immunoglobulin D.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).			
CC	-I- MISCELLANEOUS: This chain was isolated from an Igd myeloma			
CC	protein			
CC	-I- SIMILARITY: Contains 1 Ig-I-like (immunoglobulin-like) domain.			
CC	-----			
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CC	Distributed under the Creative Commons Attribution-NonDerivs License			
CC	-----			
DR	PIR; A02099; D2HUMA.			
DR	PDB; 1ZVO; X-ray; C/D=-.			
DR	SMR; P01824; 2-129.			
DR	GlycoSiteDB; P01824; -.			
DR	GO; GO:0005576; C:extracellular region; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR003599; Ig			
DR	InterPro; IPR007110; Ig-I-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	InterPro; IPR013106; V-set.			
DR	Pfam; PF07686; V-set; 1.			
DR	SMART; SMO0409; IG; 1.			
DR	SMART; SMO0406; IG; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
DR	3D-structure; Direct protein sequencing; Immunoglobulin domain;			
KW	Immunoglobulin V region.			
KW	Immunoglobulin V region.			
FT	CHAIN 1	>129		
FT				
FT				
FT	DOMAIN 1	113		
FT	NON TER 129			
FT	SEQUENCE 129 AA; 14117 MW; DSD5D347ABE51319 CRC64;			
SO				
Query Match				
	Best Local Similarity	68.9%; Score 419.5; DB 1; Length 129;		
	Matches	79; Conservative 16; Mismatches 16; Indels 15; Gaps 2;		
QY	2	ESGGLVLPKPAQTLISLCAVSGGSI	RSGGYYSWIRQHPGKLEWIGIYIHSGNTYTPNSL	61
Db	6	ESGGLVLPKPESTLSTCTVVGSGS	ISS--YVMSWIRCPAGKGLEWIGRIYISGNTYNSPL	65
QY	62	KSRIAMVDPISSENKFSRLNSVTP	ADPAVYYCA----RLGGYTLIDIGGGGLTVVSS	108
Db	66	KSRIYMSVDPISKQFSLKSSVTP	ADPAVYYCASQPMELPTVGLPTVGGGLTVVSS	123
QY	109	LTVVSS	114	





DR Pfam: PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00407; IG\_1.  
 DR SMART; SM00406; IG\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein\_65291 MM; 0D4B0776545714E CRC64;  
 SQ SEQUENCE 595 AA; 65291 MM; 0D4B0776545714E CRC64;  
 Query Match 67.2%; Score 409.5; DB 2; Length 595;  
 Best Local Similarity 66.7%; Pred. No. 5,3e-34;  
 Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;  
 QY 4 GPGLVPAQTLISLSCAVSGSIRSGGYWMIROHPGKLEWIGYIHSGNTYNPISLKS 63  
 DB 34 GAGLKPSETLSLTGCVGGSF--SGYWSWIRPQPKGLEWIGELINHGSTNYPISLKS 91  
 QY 64 RIMASVDTSENKPSLRINSVTADTAAYVYCARL-----DG-YTLDIWGCGTLVTVSS 114  
 DB 92 RVTISVDTSKKQLSLKSSVNAADTAAYVYCARVITRASPCTDGRYGMVWGCGTITVTVSS 151  
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 Q6GMX5 HUMAN PRELIMINARY; PRT; 597 AA.  
 AC 06GMX5.  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 17.  
 DE IGHM protein.  
 GN Name=IGHM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph.  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Fahy J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman A.C., Shevchenko Y., Bouffard G.G.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Lymph;  
 RC NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; BC073767; AA073767.1; -; mRNA.  
 DR SMK; Q6GMX5; 20-249.  
 DR Ensembl; ENSG00000130076; Homo sapiens.  
 DR InterPro; IPR003599; IG\_1.

DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_CL.  
 DR InterPro; IPR003066; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG\_1.  
 DR SMART; SM00407; IG\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 SQ SEQUENCE 597 AA; 65305 MM; 2A1E75F6AED85230 CRC64;  
 Query Match 67.2%; Score 409.5; DB 2; Length 597;  
 Best Local Similarity 66.7%; Pred. No. 5,3e-34;  
 Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;  
 QY 4 GPGLVPAQTLISLSCAVSGSIRSGGYWMIROHPGKLEWIGYIHSGNTYNPISLKS 63  
 DB 27 GAGLKPSETLSLTGCVGGSF--SGYWSWIRPQPKGLEWIGELINHGSTNYPISLKS 84  
 QY 64 RIMASVDTSENKPSLRINSVTADTAAYVYCARL-----DG-YTLDIWGCGTLVTVSS 114  
 DB 85 RVTISVDTSKKQLSLKSSVNAADTAAYVYCARVITRASPCTDGRYGMVWGCGTITVTVSS 144  
 RESULT 15  
 Q9BU10 HUMAN PRELIMINARY; PRT; 597 AA.  
 AC 09BU10.  
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 27.  
 DE IGHM protein.  
 GN Name=IGHM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph.  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Blakesley R.W., Touchman A.C., Shevchenko Y., Bouffard G.G.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Lymph;  
 RC NIH MGC Project;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
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? ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      81.4%; Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3,5e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

Oy      3  SGPGLVPAQCLTSCAVSGGSIKSGGYWMSIRQHPGKGLWIGYIHSNGTYNPSLK 62
Db      1  SGPGLVPSQLSLTLCITYSGSISGGHYWMSIRQHPGKGLWIGYIHSNGTYNPSLK 60

Oy      63  SRIMSVDTSENKESLRIMSVTAADTAIVYVCARLDG--YTLIDVGGTLYTVSS 114
Db      61  SRVITSDTSGNQSLSKLKSVTAADTAIVYVCARSDGSGYGGIDVWGQGTTVYSS 114

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MOELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1

```

```

; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      81.4%; Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3,5e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1.

QY      3  SGPGLVPRQAQTLSICAVSGGSIRSGGYWMIROHPGKLEWIGIYIHSQNTYINPSLK 62
      1  SGPGLVPRQAQTLSICAVSGGSIRSGGYWMIROHPGKLEWIGIYIHSQNTYINPSLK 60

QY      63  SRIMSVDTSENKSLRLNSTVADTAVYCARLDG--YTLDDINGGGLVTVSS 114
      61  SRVITISVTSKQPSLKLSTVADTAVYCARSGDYIGIDVGQGITVTVSS 114

Db

RESULT 5
US-10-330-613A-25
; Sequence 25, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudaø, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 119
TYPE: PRT
ORGANISM: Homo Sapiens

```

US-10-330-613A-25

Query Match 81.2%; Score 494.5; DB 2; Length 119;  
Best Local Similarity 82.6%; Pred. No. 3.2e-43;  
Matches 95; Conservative 8; Mismatches 9; Indels 3; Gaps 2;

QY 2 ESGPGLVKPAQTLISLCAVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLISLCTVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 65  
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCAR-LDGYTLIDWGGTLVTVSS 114  
DB 66 KSRITLSDVTSKQFSLKLNMTADTAAYYCAR-DRETAGFDYWGQGLTVTVSS 119

RESULT 6

US-10-330-613A-5  
; Sequence 5, Application US/10330613A  
; Patent No. 6924360  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613A  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613A-5

Query Match 80.4%; Score 489.5; DB 2; Length 117;  
Best Local Similarity 81.6%; Pred. No. 1e-42;  
Matches 93; Conservative 11; Mismatches 7; Indels 3; Gaps 2;

QY 2 ESGPGLVKPAQTLISLCAVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLISLCTVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 65  
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCAR-LDGYTLIDWGGTLVTVSS 114  
DB 66 KSRITLSDVTSKQFSLKLNMTADTAAYYCARGDG--KRWGGTLVTVSS 117

RESULT 7

US-09-800-729-145  
; Sequence 145, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: NI et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 145  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-729-145

Query Match 79.1%; Score 482; DB 2; Length 487;  
Best Local Similarity 74.8%; Pred. No. 3.3e-41;  
Matches 92; Conservative 12; Mismatches 9; Indels 10; Gaps 2;

QY 2 ESGPGLVKPAQTLISLCAVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 61

DB 25 ESGPGLVKPSQTLISLCTVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 84

QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCAR-LDGYTLIDWGGTLVTVSS 111

DB 85 KSRITLSDVTSKQFSLKLNMTADTAAYYCAR-DRETAGFDYWGQGLTVTVSS 144

QY 112 VSS 114  
DB 145 VSS 147

RESULT 8

US-10-330-613A-33  
; Sequence 33, Application US/10330613A  
; Patent No. 6924360  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613A  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613A-33

Query Match 78.2%; Score 476.5; DB 2; Length 117;  
Best Local Similarity 78.9%; Pred. No. 2.2e-41;  
Matches 90; Conservative 14; Mismatches 7; Indels 3; Gaps 2;

QY 2 ESGPGLVKPAQTLISLCAVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLISLCTVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 65  
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYYCAR-LDGYTLIDWGGTLVTVSS 114  
DB 66 KSRITLSDVTSKQFSLKLNMTADTAAYYCARGDG--YWGQGLTVTVSS 117

RESULT 9

US-10-330-613A-37  
; Sequence 37, Application US/10330613A  
; Patent No. 6924360  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613A  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-330-613A-37

Query Match 77.6%; Score 472.5; DB 2; Length 121;  
Best Local Similarity 76.3%; Pred. No. 5.9e-41;  
Matches 90; Conservative 13; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPAQTLISLCAVSGGSIIRSGYYWMIROHPGKLEWIGIYHSGNTYNNPSL 61

Db 6 ESGPGLVKPSETLSLCTVSGSGSIST--YYWSWIRQPKGLEWIGIYYTNTYNNPSL 63  
 QY 62 KSRVTSVDTSENKFSRLNSVTAADTAAYYCA--DINGGTLVTVSS 114  
 Db 64 KSRVTSVDTSENKFSRLNSVTAADTAAYYCAADPQWLPVPAFDIWGGTAVSVSS 121

# RESULT 10

US-08-360-125-5  
 / Sequence 5, Application US/08360125  
 / Patent No. 5767246  
 / GENERAL INFORMATION:  
 / APPLICANT: Saiko HOSOKAWA  
 / APPLICANT: Yoshiaki TAGAWA  
 / APPLICANT: Yoko HIRAKAWA  
 / APPLICANT: No. 5767246hiko ITO  
 / TITLE OF INVENTION: Human Monoclonal Antibody  
 / TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
 / TITLE OF INVENTION: Cell Membrane  
 / NUMBER OF SEQUENCES: 42  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Wenderoth, Lind & Ponack  
 / STREET: 805 Fifteenth Street, N.W., #700  
 / CITY: Washington  
 / STATE: D.C.  
 / COUNTRY: U.S.A.  
 / ZIP: 20005  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: MS-DOS  
 / SOFTWARE: WordPerfect 5.1  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/360,125  
 / FILING DATE:  
 / CLASSIFICATION: 424  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 07/905,534  
 / FILING DATE: June 29, 1992  
 / APPLICATION NUMBER:  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Warren M. Cheek, Jr.  
 / REGISTRATION NUMBER: 33,367  
 / REFERENCE/DOCKET NUMBER:  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 202-371-8850  
 / TELEFAX:  
 / TELEX:  
 / INFORMATION FOR SEQ ID NO: 5:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 119 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / HYPOTHEICAL:  
 / ANTI-SENSE:  
 / FRAGMENT TYPE:  
 / ORIGINAL SOURCE:  
 / ORGANISM:  
 / STRAIN:  
 / INDIVIDUAL ISOLATE:  
 / DEVELOPMENTAL STAGE:  
 / HAPLOTYPE:  
 / TISSUE TYPE:  
 / CELL TYPE: Hybridoma producing human  
 / CELL TYPE: antibody GAH  
 / CELL LINE:  
 / ORGANELLE:  
 / IMMEDIATE SOURCE:  
 / LIBRARY:

CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-08-360-125-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;  
 Best local Similarity 75.9%; Pred. No. 7.4e-41;  
 Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTSLSCAVSGSIRSGYYWSWIRQPKGLEWIGIYYTNTYNNPSL 61  
 Db 6 ESGPGLVKPSETLSLCTVSGSGSISCGFYNNWIRQPKGLEWIGIYYTNTYNNPSL 65  
 QY 62 KSRVTSVDTSENKFSRLNSVTAADTAAYYCA--RLDGYTLDIWGGTLVTVSS 114  
 Db 66 KSRVTSVDTSENKFSRLNSVTAADTAAYYCA--ADYVGGTAVSVSS 119

# RESULT 11

US-08-450-578-5  
 / Sequence 5, Application US/08450578  
 / Patent No. 5837845  
 / GENERAL INFORMATION:  
 / APPLICANT: Saiko HOSOKAWA  
 / APPLICANT: Yoshiaki TAGAWA  
 / APPLICANT: Yoko HIRAKAWA  
 / APPLICANT: No. 5837845hiko ITO  
 / TITLE OF INVENTION: Human Monoclonal Antibody  
 / TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
 / TITLE OF INVENTION: Cell Membrane  
 / NUMBER OF SEQUENCES: 42  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Wenderoth, Lind & Ponack  
 / STREET: 805 Fifteenth Street, N.W., #700  
 / CITY: Washington  
 / STATE: D.C.  
 / COUNTRY: U.S.A.  
 / ZIP: 20005  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: MS-DOS  
 / SOFTWARE: WordPerfect 5.1  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/450,578  
 / FILING DATE: May 25, 1995  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/360,125  
 / FILING DATE: December 20, 1994  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 07/905,534  
 / FILING DATE: June 29, 1992



ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human  
CELL LINE:  
ORGANELL:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-450-578-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.4e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGSIRSGYYWSMIRHFGKLEWIGYIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLISLCTVSGGSISGCFYWMIRHFGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTVSS 114  
DB 66 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTVSS 119

RESULT 12  
US-09-017-628-5  
Sequence 5, Application US/09017628  
Patent No. 5990287  
GENERAL INFORMATION:

APPLICANT: HOSOKAWA, Saiko  
APPLICANT: TAGAWA, Yoshiaki  
APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITO, No. 5990287ihiko  
APPLICANT: NAGAIKE, Kazuhiro  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO  
FILE REFERENCE: 177/527361KH  
CURRENT APPLICATION NUMBER: US/09/017,628  
CURRENT FILING DATE: 1998-02-02  
EARLIER APPLICATION NUMBER: 08/360,125  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.4e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGSIRSGYYWSMIRHFGKLEWIGYIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLISLCTVSGGSISGCFYWMIRHFGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTVSS 114  
DB 66 KSRVITSLDTSKQSFSLKSLSLTAADTAAYYCARSTRLRG--ADYWGQGTMTVSS 119

RESULT 13  
US-09-014-880-5  
Sequence 5, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 203 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human  
CELL TYPE: antibody GAH  
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;  
Best Local Similarity 75.9%; Pred. No. 7.4e-41;  
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYWSWIRHPGKLEWIGYIYHSGNTYVNSL 61  
Db 6 ESGPGLVKPSETSLTCTVSGGSISCGFTWMIROHPGKLEWIGYIYHSGNTYVNSL 65

Qy 62 KSRITAMSVDTSENKFSRLNSVTADTAVYYCARLDG---YTLDDIWGGTLVTYSS 114  
Db 66 KSRITISLDTSKQFSLKLSSTLTADTAVYYCARSTRLRG--ADYWGQGTMTYVSS 119

RESULT 14  
US-09-025-769B-39  
Sequence 39, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-025-769B-39

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 77.6%; Pred. No. 7.4e-41;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYWSWIRHPGKLEWIGYIYHSGNTYVNSL 61  
Db 6 ESGPGLVKPSETSLTCTVSGGSIS--YVWSWIRHPGKLEWIGYIYHSGNTYVNSL 63

Qy 62 KSRITAMSVDTSENKFSRLNSVTADTAVYYCARLDG---YTLDDIWGGTLVTYSS 114  
Db 64 KSRITISLDTSKQFSLKLSSTLTADTAVYYCARWGSDGFYADYWGQGTMTYVSS 119

RESULT 15  
US-09-025-769B-65  
Sequence 65, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-65

Query Match 77.4%; Score 471.5; DB 2; Length 119;  
Best Local Similarity 77.6%; Pred. No. 7.4e-41;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYWSWIRHPGKLEWIGYIYHSGNTYVNSL 61  
Db 6 ESGPGLVKPSETSLTCTVSGGSIS--YVWSWIRHPGKLEWIGYIYHSGNTYVNSL 63

Qy 62 KSRITAMSVDTSENKFSRLNSVTADTAVYYCARLDG---YTLDDIWGGTLVTYSS 114  
Db 64 KSRITISLDTSKQFSLKLSSTLTADTAVYYCARWGSDGFYADYWGQGTMTYVSS 119

Search completed: August 30, 2006, 00:37:11  
Job time : 16.5455 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 65.2909 Seconds  
(without alignments)  
808.788 Million cell updates/sec

Title: US-10-027-725A-7  
Perfect score: 609  
Sequence: 1 LBSGPELVPAQTLISLSCAV.....RLDGYTLDIWGQTLVTSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ProdData/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ProdData/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ProdData/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ProdData/2/pubppaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ProdData/2/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ProdData/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	609	100.0	114	US-10-027-725A-7	Sequence 7, Appl1
2	556	91.3	114	US-10-027-725A-9	Sequence 9, Appl1
3	546	89.7	114	US-10-027-725A-8	Sequence 8, Appl1
4	519	85.2	122	US-10-309-762-147	Sequence 147, Appl1
5	518.5	85.1	121	US-10-309-762-152	Sequence 152, Appl1
6	517.5	85.0	125	US-10-309-762-11	Sequence 11, Appl1
7	514.5	84.5	121	US-10-309-762-151	Sequence 151, Appl1
8	512	84.1	118	US-10-309-762-138	Sequence 138, Appl1
9	512	84.1	120	US-10-309-762-13	Sequence 13, Appl1
10	512	84.1	120	US-10-309-762-144	Sequence 144, Appl1
11	509.5	83.7	123	US-10-309-762-12	Sequence 12, Appl1
12	509.5	83.7	123	US-11-131-648-13	Sequence 13, Appl1
13	509.5	83.7	123	US-11-131-648-13	Sequence 13, Appl1
14	508.5	83.5	123	US-10-309-762-10	Sequence 35, Appl1
15	508.5	83.5	123	US-10-309-762-18	Sequence 10, Appl1
16	508.5	83.5	123	US-10-309-762-19	Sequence 18, Appl1
17	508.5	83.5	125	US-10-309-762-8	Sequence 19, Appl1
18	508.5	83.5	125	US-10-309-762-16	Sequence 8, Appl1
19	508.5	83.5	125	US-10-309-762-16	Sequence 16, Appl1
20	506.5	83.2	119	US-10-309-762-131	Sequence 35, Appl1
21	505.5	83.0	119	US-10-309-762-131	Sequence 131, Appl1
22	505	82.9	252	US-09-880-748-1994	Sequence 140, Appl1
23	505	82.9	252	US-10-293-418-1994	Sequence 1994, Appl1
24	505	82.9	252	US-11-054-515-1994	Sequence 1994, Appl1
25	505	82.9	252	US-11-266-444-1994	Sequence 1994, Appl1
26	504.5	82.8	125	US-10-309-762-153	Sequence 153, Appl1
27	504.5	82.8	480	US-10-910-901-6	Sequence 6, Appl1

28	504	82.8	120	US-10-309-762-139	Sequence 139, Appl1
29	503.5	82.7	127	US-10-309-762-14	Sequence 14, Appl1
30	503	82.6	124	US-10-309-762-75	Sequence 75, Appl1
31	503	82.6	143	US-10-309-762-96	Sequence 96, Appl1
32	501.5	82.3	117	US-10-330-613-13	Sequence 13, Appl1
33	501.5	82.3	117	US-10-330-530-13	Sequence 13, Appl1
34	501.5	82.3	117	US-10-660-357-13	Sequence 13, Appl1
35	501	82.3	149	US-10-910-901-22	Sequence 22, Appl1
36	500.5	82.2	123	US-10-893-576-190	Sequence 190, Appl1
37	500.5	82.2	251	US-10-120-414-75	Sequence 75, Appl1
38	500.5	82.2	251	US-10-992-195-75	Sequence 75, Appl1
39	500	82.1	125	US-10-805-177-53	Sequence 53, Appl1
40	498.5	81.9	253	US-09-880-748-1619	Sequence 1619, Appl1
41	498.5	81.9	253	US-10-293-418-1619	Sequence 1619, Appl1
42	498.5	81.9	253	US-11-054-515-1619	Sequence 1619, Appl1
43	498.5	81.9	253	US-11-266-444-1619	Sequence 1619, Appl1
44	497.5	81.7	148	US-10-893-576-31	Sequence 31, Appl1
45	497	81.6	110	US-10-309-762-74	Sequence 74, Appl1

## ALIGNMENTS

```
RESULT 1
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match      100.0% Score 609; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.7e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LBSGPELVPAQTLISLSCAVSGSIRSGYWSWIRHFGKLEWIGYTHSGNTYNS 60
      |||||
DB      1 LBSGPELVPAQTLISLSCAVSGSIRSGYWSWIRHFGKLEWIGYTHSGNTYNS 60
      |||||
QY      61 LKSRIMSVDTSEKRSFLNSVTADTVVYCARLDGYTLDIWGQTLVTSS 114
      |||||
DB      61 LKSRIMSVDTSEKRSFLNSVTADTVVYCARLDGYTLDIWGQTLVTSS 114
      |||||

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
```

ORGANISM: Homo sapiens  
US-10-027-725A-9

Query Match	91.3%;	Score 556;	DB 4;	Length 114;
Best Local Similarity	90.4%;	Pred. No. 5.7e-44;		
Matches 103; Conservative	5;	Mismatches 6;	Indels 0;	Gaps 0;

**Qy**

1 LESGPGIVKPAOTLSLSCAVSGSIRSGGYWSWIRQHPEKGLENIGIYHSGNTYYNPS 600  
||||| : |||| : |||||  
**Db**

1 LESGPGIVKPSOTLSLTCTVSGGSIRSGGYWSWIRQPFGKLENIICYIHSGNTYYNPS 600

```
Oy      61 LKSR IAMSVDTS ENKFSLRLNSVTAADTAVYYCARLDGVTLPDINGQGTLYTVSS 114
        ||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      61 LKSRTMSVDTSKNHFSLRLLSSVTAADTAVYYCARSDGYTLDDNWGGTLYTVSS 114
```

RESULT 3  
US-10-027-725A-8

Publication No. US20030082659A1  
GENERAL INFORMATION:  
APPLICANT: Flicker, Sabine  
TITLE OF INVENTION: System and method for providing a user interface for a user interface

```

; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436

```

```

; PRIOR FILING DATE: 2000-12-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8

```

```

/      LENGTH: 117
;      TYPE: PRT
;      ORGANISM: Homo sapiens
US-10-027-725A-8

```

Query Match	89.7%;	Score 546;	DB 4;	Length 114;
Best Local Similarity	89.5%;	Pred. No. 4.8e-43;		
Matches 102; Conservative	4;	Mismatches 8;	Indels 0;	Gaps 0;

```

Oy      1  LBSGPGLVKPAQTLTSLSCAVSGSIRSGGYWMSWIRHOPGKLEWIGIYIYHSGNTYYNN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1  LBSGPGLVKPSQTLTSLCTVSGSIRSGGYWMSWIRQPPGKLEWIGNIYHSGNTYYNN

```

```

Oy      61 LKSRITMSVDTSKNHFSRLTSTYTAADTA VYVCARSDGYTLIDNWGGSTLVYSS 114
        ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 LKSRITMSVDTSKNHFSRLTSTYTAADTA VYVCARSDGYTLIDNWGGSTLVYSS 114

```

RESULT 4  
US-10-309-762-147

Query Match	85.2%;	Score 519;	DB 4;	Length 122;
Best Local Similarity	81.2%;	Pred. No. 1.7e-40;		
Matches 95;	Conservative 12;	Mismatches 6;	Indels 4;	Gaps 1

QY 2 ESGPELVKPAQTLSLSCAVSGSIRSGGYWMSIRQHPEKGLEWIGIYHSNGTYNPSL 61  
| | | | | : | | | | | | | | | | | | | | | | | | | | | |  
DB 6 ESGPELVKPSQTLSTCTVSGGSISSGGYWMSIRQHPEKGLEWIGIYYSGSYYNPSL 65

QY 62 KSRIRAMSVPTSENKRFSLRNSTTAADPAVYYCAR----LDGYTIDIMGQGTLTVASS 114  
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||  
Db 66 KSRVTISVDTSKNQFSLKLSSVTAAADPAVYYCARYYDILTGYGDMDVGQGITTIVASS 122

RESULT 5  
US-10-309-762-152  
Commerce 152 Application US/10309762

```

; PUBLICATION NO. US20040018196A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Gudas, Jean
;
; APPLICANT: Foltz, Jan

```

AFFILIANT: natia, masaba  
 APPLICANT: Gallo, Michael  
 TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
 TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

```

CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275

```

```

;      NUMBER OF SEQ ID NOS: 246
;
;      SOFTWARE: FastSeq for Windows Version 4.0
;
;      SEQ ID NO 152

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

```

Query Match	85.1%;	Score 518.5;	DB 4;	Length 121;
Best Local Similarity	81.9%;	Pred. No. 1.8e-40;		
Matches 95; Conservative	11;	Mismatches 7;	Indels 3;	Gaps

```

QY      2  ESGPGLVKPAQTLISLCAVSGGSIRSGCYWWSWIRQHPGKGLEWIGYIYHSNTYINPSL 6
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      6  ESGPGLVKPQSTLSLCTVSGGSISSGGYWSWIRQHPGKGLEWIGYIYISGSTYINPSL 6

```

```

62 KSRIMNSVDTSNKKFSLRLNSVTADIAIVYCARLD---SYTIDJWGQGLIVVSS 114
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
66 KSRVITISVDTSKQFSLKLISSVTADIAIVYCAIYDILITGYAFDIWGQGLIVVSS 121

```

Query Match	85.0%	Score 517.5;	DB 4;	length 125;
Best Local Similarity	81.7%;	Pred. No. 2.4e-40;		
Matches 98;	Conservative 9;	Mismatches 6;	Indels 7;	Gaps 2;

QY 2 ESPPGLVAKPAQATLSLSICAVSGSIRSGGYMSWIRQHGKGLBMYGYHSGNTYINPST 61

Db 6 ESPPGLVAKPSQTLTLCTVSSGGSSISGGYMSWIRQHGKGLBMYGYHSGNTYINPST 65

QY 62 KASIANSVDTSENKPELRINSVTAADPLVYCAR-----LDGY--TLIDISQGLTLVYSS 114

Db 66 KSRITTSVDTSKQPSLKLSVTAADPLVYCARITTYPLFLGYPAEDISQGLTNVYSS 1253

```

RESULT 7
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudaas, Dean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX, 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-309-762-151

```

[illegible]

```

1 RESULT 8
2 US-10-309-762-138
3
4 ; Sequence 138, Application US/10309762
5 ; Publication No. US20040018198A1
6 ;
7 ; GENERAL INFORMATION:
8 ;
9 ; APPLICANT: Gudas, Jean
10 ; APPLICANT: Poltz, Ian
11 ; APPLICANT: Hands, Masahisa
12 ; APPLICANT: Gallo, Michael
13 ;
14 ; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
15 ;
16 ; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
17 ;
18 ; FILE REFERENCE: ABGENIX.027A
19 ;
20 ; CURRENT APPLICATION NUMBER: US/10/309,762
21 ;
22 ; CURRENT FILING DATE: 2002-12-02
23 ;
24 ; PRIOR APPLICATION NUMBER: 60/337215
25 ;
26 ; PRIOR FILING DATE: 2001-12-03
27 ;
28 ; NUMBER OF SEQ ID NOS: 246
29 ;
30 ; SOFTWARE: FastSeq for Windows Version 4.0
31 ;
32 ; SEQ ID NO 138
33 ;
34 ; LENGTH: 118
35 ;
36 ; TYPE: PRT
37 ;
38 ; ORGANISM: Homo sapiens
39 ;

```

```

US-10-309-762-138

Query Match      84.1%; Score 512; DB 4; Length 118;
Best Local Similarity 83.2%; Pred. No. 7.2e-40;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
```

[illegible]

```

RESULT 9
US-10-309-762-13
Sequence 13, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE 1X
FILE REFERENCE: ARGENIX 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: FRT
ORGANISM: Homo sapiens
US-10-309-762-13

```

[illegible]

```

, RESULT 10
, US-10-309-762-144
, Sequence 144, Application US/10309762
, Publication No. US20040018198A1
, GENERAL INFORMATION:
, APPLICANT: Gudas, Jean
, APPLICANT: Foltz, Ian
, APPLICANT: Handa, Masahisa
, APPLICANT: Gallo, Michael
, TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
, TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
, FILE REFERENCE: AGENIX.027A
, CURRENT APPLICATION NUMBER: US/10/309,762
, CURRENT FILING DATE: 2002-12-02
, PRIOR APPLICATION NUMBER: 60/337275
, PRIOR FILING DATE: 2001-12-03
, NUMBER OF SEQ ID NOS: 246
, SOFTWARE: SEQSEQ for Windows Version 4.0
, SEQ ID NO 144
, LENGTH: 120
, TYPE: PRT
,

```

ORGANISM: Homo sapiens  
US-10-309-762-144

Query Match 84.1%; Score 512; DB 4; Length 120;  
Best Local Similarity 81.9%; Pred. No. 7,4e-40;  
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVPAQTSLSCAVSGSIRSGYWSWIRHPKGLKLEWIGYIYHSGNTYVPSL 61  
DB 6 ESGPGLVPAQTSLSCAVSGSIRSGYWSWIRHPKGLKLEWIGYIYHSGNTYVPSL 65  
QY 62 KSRIVSVDTSENKFSRLNSVTADTAVYYCARLDGVT---LDIMQGLTVTVSS 114  
DB 66 KSRIVSVDTSENKFSRLNSVTADTAVYYCAR-DGYNWYFPLWGRGLTVTVSS 120

RESULT 11

US-10-309-762-12  
Sequence 12, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Folcz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: AGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-12

Query Match 83.7%; Score 509.5; DB 4; Length 123;  
Best Local Similarity 78.8%; Pred. No. 1.3e-39;  
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

QY 2 ESGPGLVPAQTSLSCAVSGSIRSGYWSWIRHPKGLKLEWIGYIYHSGNTYVPSL 61  
DB 6 ESGPGLVPAQTSLSCAVSGSIRSGYWSWIRHPKGLKLEWIGYIYHSGNTYVPSL 65  
QY 62 KSRIVSVDTSENKFSRLNSVTADTAVYYCARL-----DGYTLIDIMQGLTVTVSS 114  
DB 66 KSRIVSVDTSENKFSRLNSVTADTAVYYCARLVMFGEDYVDWVGCGTVTVSS 123

RESULT 12

US-11-131-648-13  
Sequence 13, Application US/11131648  
Publication No. US20050221400A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Jakobovits, Aya  
APPLICANT: Xiao-Chi, Jia  
APPLICANT: Morrison, Robert Kendall  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Shao, Hui  
APPLICANT: Chailita-Eid, Pia M.  
APPLICANT: Raitano, Arthur B.  
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS  
FILE REFERENCE: 51158-20088.20  
CURRENT APPLICATION NUMBER: US/11/131,648  
CURRENT FILING DATE: 2005-05-17  
PRIOR APPLICATION NUMBER: 60/616,381  
PRIOR FILING DATE: 2004-10-05  
PRIOR APPLICATION NUMBER: 60/617,881

PRIOR FILING DATE: 2004-10-12  
PRIOR APPLICATION NUMBER: 60/621,310  
PRIOR FILING DATE: 2004-10-21  
PRIOR APPLICATION NUMBER: 60/633,077  
PRIOR FILING DATE: 2004-12-02  
PRIOR APPLICATION NUMBER: 10/857,484  
PRIOR FILING DATE: 2004-05-28  
PRIOR APPLICATION NUMBER: 60/475,064  
PRIOR FILING DATE: 2003-05-30  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 148  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-131-648-13

Query Match 83.7%; Score 509.5; DB 6; Length 148;  
Best Local Similarity 78.5%; Pred. No. 1.6e-39;  
Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;

QY 2 ESGPGLVPAQTSLSCAVSGSIRSGYWSWIRHPKGLKLEWIGYIYHSGNTYVPSL 61  
DB 15 ESGPGLVPAQTSLSCAVSGSIRSGYWSWIRHPKGLKLEWIGYIYHSGNTYVPSL 74  
QY 62 KSRIVSVDTSENKFSRLNSVTADTAVYYCARLDGVT-----YTLIDIMQGLTVTVS 113  
DB 75 KSRIVSVDTSENKFSRLNSVTADTAVYYCAR-DGYNWYFPLWGRGLTVTVS 133  
QY 114 S 114  
DB 134 S 134

RESULT 13

US-11-131-648-35  
Sequence 35, Application US/11131648  
Publication No. US20050221400A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Jakobovits, Aya  
APPLICANT: Xiao-Chi, Jia  
APPLICANT: Morrison, Robert Kendall  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Shao, Hui  
APPLICANT: Chailita-Eid, Pia M.  
APPLICANT: Raitano, Arthur B.  
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS  
FILE REFERENCE: 51158-20088.20  
CURRENT APPLICATION NUMBER: US/11/131,648  
CURRENT FILING DATE: 2005-05-17  
PRIOR APPLICATION NUMBER: 60/616,381  
PRIOR FILING DATE: 2004-10-05  
PRIOR APPLICATION NUMBER: 60/617,881  
PRIOR FILING DATE: 2004-10-12  
PRIOR APPLICATION NUMBER: 60/621,310  
PRIOR FILING DATE: 2004-10-21  
PRIOR APPLICATION NUMBER: 60/633,077  
PRIOR FILING DATE: 2004-12-02  
PRIOR APPLICATION NUMBER: 10/857,484  
PRIOR FILING DATE: 2004-05-28  
PRIOR APPLICATION NUMBER: 60/475,064  
PRIOR FILING DATE: 2003-05-30  
NUMBER OF SEQ ID NOS: 78  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 35  
LENGTH: 148  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-131-648-35

Query Match 83.7%; Score 509.5; DB 6; Length 148;  
Best Local Similarity 78.5%; Pred. No. 1.6e-39;



```
Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;
QY 2 ESGPGLVKPAQTLSLCAVSGSIRSGYYWMIROHPGKGLWIGIYHSGNTYYNPSL 61
DB 15 ESGPGLVKPSQTLSTCTVSGSSISGGYYWMIROHPGKGLWIGIYHSGNTYYNPSL 74
QY 62 KSRIANSVDTSENKFSRLNSVTADTAAYYCARLPG-----YTLDDIWGGTLVTVSS 113
DB 75 KSRVITSVDTSENKQFSLKLSVTADTAAYYCAR-DGIMIRGYYGMDVWGQGTIVTVSS 133
QY 114 S 114
DB 134 S 134

RESULT 14
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match 83.5%; Score 508.5; DB 4; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.6e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
QY 2 ESGPGLVKPAQTLSLCAVSGSIRSGYYWMIROHPGKGLWIGIYHSGNTYYNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSSISGGYYWMIROHPGKGLWIGIYHSGNTYYNPSL 65
QY 62 KSRIANSVDTSENKFSRLNSVTADTAAYYCARLPG-----YTLDDIWGGTLVTVSS 114
DB 66 KSRVITSVDTSENKQFSLKLSVTADTAAYYCARAGKRYGSGSYLDVWGQGTIVTVSS 123

RESULT 15
US-10-309-762-18
; Sequence 18, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
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```
; ORGANISM: Homo sapiens
US-10-309-762-18

Query Match 83.5%; Score 508.5; DB 4; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.6e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
QY 2 ESGPGLVKPAQTLSLCAVSGSIRSGYYWMIROHPGKGLWIGIYHSGNTYYNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSSISGGYYWMIROHPGKGLWIGIYHSGNTYYNPSL 65
QY 62 KSRIANSVDTSENKFSRLNSVTADTAAYYCARLPG-----YTLDDIWGGTLVTVSS 114
DB 66 KSRVITSVDTSENKQFSLKLSVTADTAAYYCARERVTDDYYGGLDWGQGTIVTVSS 123

Search completed: August 30, 2006, 00:50:41
Job time : 66.2909 secs
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 13.4727 Seconds  
(without alignments)  
578.960 Million cell updates/sec

Title: US-10-027-725a-7

Sequence: 1 EESGPGLVKPAQTLISLSCAV.....RLDGYTLIDWGGTLVTWSS 114  
Perfect score: 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US09\_NEW\_PUB pep:\*
- 2: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US06\_NEW\_PUB pep:\*
- 3: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US07\_NEW\_PUB pep:\*
- 4: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US08\_NEW\_PUB pep:\*
- 5: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/PCT\_NEW\_PUB pep:\*
- 6: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US10\_NEW\_PUB pep:\*
- 7: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US11\_NEW\_PUB pep:\*
- 8: /EMC\_Celerra\_SIDS3/Ptodata/2/pubppa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509.5	83.7	118	US-10-981-300-51	Sequence 51, App1
2	493.5	81.0	149	US-11-355-464-13	Sequence 13, App1
3	493.5	81.0	149	US-11-355-464-16	Sequence 16, App1
4	479.5	78.7	118	US-10-981-300-52	Sequence 52, App1
5	479.5	78.7	180	US-10-981-300-4	Sequence 4, App1
6	474	77.8	247	US-10-539-402-10	Sequence 10, App1
7	471.5	77.4	119	US-11-304-986-25	Sequence 25, App1
8	467.5	76.8	121	US-11-211-917-98	Sequence 98, App1
9	467.5	76.8	121	US-11-211-917-70	Sequence 70, App1
10	465.5	76.4	121	US-11-211-917-66	Sequence 66, App1
11	463	76.0	126	US-10-994-679-68	Sequence 68, App1
12	462.5	75.9	121	US-11-211-917-82	Sequence 82, App1
13	462.5	75.9	121	US-11-211-917-86	Sequence 86, App1
14	462	75.9	115	US-10-981-300-53	Sequence 53, App1
15	462	75.9	120	US-11-281-266-6	Sequence 6, App1
16	459.5	75.5	121	US-11-337-300-84	Sequence 84, App1
17	459.5	75.5	248	US-11-337-300-94	Sequence 94, App1
18	456	74.9	118	US-11-211-917-109	Sequence 109, App1
19	454	74.5	118	US-11-211-917-142	Sequence 142, App1
20	451.5	74.1	118	US-10-981-300-54	Sequence 54, App1
21	451.5	74.1	443	US-10-981-300-20	Sequence 20, App1
22	450	73.9	108	US-11-281-266-82	Sequence 82, App1
23	450	73.9	120	US-11-211-917-108	Sequence 108, App1
24	448.5	73.6	121	US-11-211-917-26	Sequence 26, App1
25	448.5	73.6	466	US-11-211-917-30	Sequence 30, App1

26	446.5	73.3	107	US-10-484-105-18	Sequence 18, App1
27	445.5	73.2	113	US-11-290-687-17	Sequence 17, App1
28	445	73.1	244	US-11-402-010-77	Sequence 77, App1
29	444.5	73.0	119	US-11-211-917-18	Sequence 18, App1
30	444.5	73.0	464	US-11-211-917-22	Sequence 22, App1
31	442.5	72.7	121	US-10-994-679-60	Sequence 60, App1
32	440	72.2	112	US-11-249-296-64	Sequence 64, App1
33	435	71.4	108	US-11-281-266-85	Sequence 85, App1
34	435	71.4	112	US-11-249-296-68	Sequence 68, App1
35	434	71.3	247	US-10-539-402-15	Sequence 15, App1
36	433	71.1	286	US-11-354-103-8	Sequence 8, App1
37	432	70.9	244	US-11-317-786B-17	Sequence 17, App1
38	432	70.9	448	US-11-317-786B-9	Sequence 9, App1
39	431	70.8	124	US-11-111-688-3	Sequence 3, App1
40	431	70.8	130	US-11-111-688-58	Sequence 58, App1
41	430.5	70.7	127	US-11-259-133-202	Sequence 202, App
42	430	70.6	240	US-11-317-786B-15	Sequence 15, App1
43	430	70.6	445	US-11-317-786B-32	Sequence 32, App1
44	430	70.6	448	US-11-317-786B-7	Sequence 7, App1
45	429	70.4	124	US-11-111-688-1	Sequence 1, App1

#### ALIGNMENTS

RESULT 1  
US-10-981-300-51  
Sequence 51, Application US/10981300  
Publication No. US2006009359A1  
GENERAL INFORMATION:  
APPLICANT: GIORGIO SENALDI  
APPLICANT: GADI GAZIT-BORSTEIN  
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
FILE REFERENCE: ABGX-005  
CURRENT APPLICATION NUMBER: US/10/981,300  
CURRENT FILING DATE: 2004-11-03  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PaateSeq for Windows Version 4.0  
SEQ ID NO 51  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-981-300-51

Query Match 83.7%; Score 509.5; DB 6; Length 118;  
Best Local Similarity 83.2%; Pred. No. 1.1e-40;  
Matches 94; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 2 EESGPGLVKPAQTLISLSCAVSGSIRSGYYWMIROHPGKLEWIGYIHSGTYNPSL 61  
DB 6 EESGPGLVKPSQTLISLCTVSGSGSYWMIROHPKGLWIGYIYSGSTYINPSL 65  
QY 62 KSRIVSVTSNKQFSLRLNSVTADTAVYCCARLDGYTLIDWGGTLVTWSS 114  
DB 66 KSRVITSVTSNKQFSLKLSVTADTAVYCCARTGDYFDVWGGTLVTWSS 117

RESULT 2  
US-11-355-464-13  
Sequence 13, Application US/11355464  
Publication No. US20060147375A1  
GENERAL INFORMATION:  
APPLICANT: GUDAS, Uean  
APPLICANT: JAKOBOWITS, Aya  
APPLICANT: JIA, Xiao-Chi,  
APPLICANT: MORRISON, Robert Kendall,  
APPLICANT: CHALILITA-EID, Pia M.  
APPLICANT: RAITANO, Arthur B.  
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT  
TITLE OF INVENTION: BIND TO PSCA PROTEINS  
FILE REFERENCE: 511582008821  
CURRENT APPLICATION NUMBER: US/11/355,464

```

; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US 11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-355-464-13
```

```

Query Match      81.0%; Score 493.5; DB 7; Length 149;
Best Local Similarity 76.9%; Pred. No. 4.2e-39;
Matches 93; Conservative 12; Mismatches 7; Indels 9; Gaps 2;
```

```

QY      2  ESGPGLVKPAQTLSLCAVSGSIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 61
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4  ESGPGLVKPSQTLSTCTVSGSISGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 63
QY      62  KSRIVSVDTSENKESLRINSVTADTAAYYCARLDGYT-----LDIWGGTLVTVS 113
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64  KSRVITISVDTSKQPSLKLSTSGTAADTAAYYCAR-DHITWVRGVPKGMVWGQGITVTVS 122
QY      114 S 114
Db      123 S 123
```

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RESULT 3
US-11-355-464-16
; Sequence 16, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: CHALILITA-RID, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT APPLICATION NUMBER: US/11/355,464
; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US 11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
```

```

; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-355-464-16
```

```

Query Match      81.0%; Score 493.5; DB 7; Length 149;
Best Local Similarity 76.9%; Pred. No. 4.2e-39;
Matches 93; Conservative 12; Mismatches 7; Indels 9; Gaps 2;
```

```

QY      2  ESGPGLVKPAQTLSLCAVSGSIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 61
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      4  ESGPGLVKPSQTLSTCTVSGSISGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 63
QY      62  KSRIVSVDTSENKESLRINSVTADTAAYYCARLDGYT-----LDIWGGTLVTVS 113
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64  KSRVITISVDTSKQPSLKLSTSGTAADTAAYYCAR-DHITWVRGVPKGMVWGQGITVTVS 122
QY      114 S 114
Db      123 S 123
```

```

RESULT 4
US-10-981-300-52
; Sequence 52, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-981-300-52
```

```

Query Match      78.7%; Score 479.5; DB 6; Length 118;
Best Local Similarity 78.8%; Pred. No. 6.8e-38;
Matches 89; Conservative 11; Mismatches 12; Indels 1; Gaps 1;
```

```

QY      2  ESGPGLVKPAQTLSLCAVSGSIRSGGYWSWIRHPGKLEWIGIYHSGNTYNNPSL 61
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  QSGPGLVKPSQTLSTCTVSGSDISSGHHWSWIRHPGKLEWIGIYHSGNTYNNPSL 65
QY      62  KSRIVSVDTSENKESLRINSVTADTAAYYCARLDGYTLDIWGGTLVTVS 114
         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRFTISVDTSKQPSLKLSTSGTAADTAAYYCARLDGYTLDIWGGTLVTVS 117
```

```

RESULT 5
US-10-981-300-4
; Sequence 4, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 4  
LENGTH: 180  
TYPE: PRT  
ORGANISM: homo sapien  
US-10-981-300-4

Query Match 78.7%; Score 479.5; DB 6; Length 180;  
Best Local Similarity 78.8%; Pred. No. 1e-37;  
Matches 89; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 2 ESGPGLVKAQTLISLCAVSGGSIIRSGGYWMIROHPGKGLMIGIYHSGNTYNNPSL 61  
DB 6 QSGPGLVKAQTLISLCTVSGDSISSGCHYWSMIRQHPGKGLMIGIYHSGNTYNNPSL 65

QY 62 KSRIVSVPTSENKFSRLNLSVTAADTAVYYCARLDGTYLIDINGQGLTVTVSS 114  
DB 66 KSRVITSVPTSKNPSLKLSTVTAADTAVYYCARLTDY-PDYWGGLGLTVTVSS 117

RESULT 6  
US-10-539-402-10  
Sequence 10, Application US/10539402  
Publication No. US20060115477A1  
GENERAL INFORMATION:  
APPLICANT: Xerion Pharmaceuticals AG  
APPLICANT: Tufts University  
TITLE OF INVENTION: Neuropilin-1 Inhibitor  
FILE REFERENCE: XE12BPC  
CURRENT APPLICATION NUMBER: US/10/539,402  
CURRENT FILING DATE: 2005-06-17  
PRIOR APPLICATION NUMBER: US 60/435,893  
PRIOR FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: EP 03000615  
PRIOR FILING DATE: 2003-01-15  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 247  
TYPE: PRT  
ORGANISM: human  
US-10-539-402-10

Query Match 77.8%; Score 474; DB 6; Length 247;  
Best Local Similarity 75.7%; Pred. No. 4.6e-37;  
Matches 87; Conservative 16; Mismatches 6; Indels 6; Gaps 2;

QY 4 GPGIVKPAQTLISLCAVSGGSIIRSGGYWMIROHPGKGLMIGIYHSGNTYNNPSL 63  
DB 9 GPGIVKASETILSLCTVSGSSLSGGYWSMIRQHPGKGLMIGIYHSGNTYNNPSL 68

QY 64 RIMSVPTSENKFSRLNLSVTAADTAVYYCARL---DGYTLIDINGQGLTVTVSS 114  
DB 69 RIVITSVPTSKNPSLKLSTVTAADTAVYYCARVPLRPDGF--DVGQGLTVTVSS 121

RESULT 7  
US-11-304-986-25  
Sequence 25, Application US/11304986  
Publication No. US20060165682A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth and NeutraLab et al.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA  
TITLE OF INVENTION: AMYLOID PEPTIDE  
FILE REFERENCE: ELN-055  
CURRENT APPLICATION NUMBER: US/11/304,986  
CURRENT FILING DATE: 2005-12-15  
PRIOR APPLICATION NUMBER: 60/636684  
PRIOR FILING DATE: 2004-12-15  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 119  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic construct, consensus sequence for heavy chain  
OTHER INFORMATION: framework region  
US-11-304-986-25

Query Match 77.4%; Score 471.5; DB 7; Length 119;  
Best Local Similarity 77.6%; Pred. No. 3.8e-37;  
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGLVKAQTLISLCAVSGGSIIRSGGYWMIROHPGKGLMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKAQTLISLCTVSGGSIIR--GYWSMIRQHPGKGLMIGIYHSGNTYNNPSL 63

QY 62 KSRIVSVPTSENKFSRLNLSVTAADTAVYYCARLDG---YTLIDINGQGLTVTVSS 114  
DB 64 KSRVITSVPTSKNPSLKLSTVTAADTAVYYCARWGSDGDFYANDYWGQGLTVTVSS 119

RESULT 8  
US-11-211-917-98  
Sequence 98, Application US/11211917  
Publication No. US20060093600A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 98  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-211-917-98

Query Match 76.8%; Score 467.5; DB 7; Length 121;  
Best Local Similarity 77.1%; Pred. No. 9.2e-37;  
Matches 91; Conservative 10; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESGPGLVKAQTLISLCAVSGGSIIRSGGYWMIROHPGKGLMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKAQTLISLCTVSGGSIIR--GYWSMIRQHPGKGLMIGIYHSGNTYNNPSL 63

QY 62 KSRIVSVPTSENKFSRLNLSVTAADTAVYYCARLDGTYLID---WGQGLTVTVSS 114  
DB 64 KSRVITSVPTSKNPSLKLSTVTAADTAVYYCARKGLVGDYGMFAPWGQGLTVTVSS 121

RESULT 9  
US-11-211-917-70  
Sequence 70, Application US/11211917  
Publication No. US20060093600A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088

;; PRIOR FILING DATE: 2002-11-08  
;; PRIOR APPLICATION NUMBER: 60/348,980  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 70  
;; LENGTH: 466  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-211-917-70

Query Match 76.8%; Score 467.5; DB 7; Length 466;  
Best Local Similarity 77.1%; Pred. No. 3.5e-36;  
Matches 91; Conservative 10; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 61  
DB 25 ESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 82  
QY 62 KSRVTISVDTSKQFSLKLSNVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 114  
DB 83 KSRVTISVDTSKQFSLKLSNVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 140

RESULT 10  
US-11-211-917-66  
;; Sequence 66, Application US/11211917  
;; Publication No. US2006093600A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BEDIAN, VAHE  
;; APPLICANT: GLADUE, RONALD P.  
;; APPLICANT: CORVALAN, JOSE  
;; APPLICANT: JIA, XIAO-CHI.  
;; APPLICANT: FENG, XIAO  
;; TITLE OF INVENTION: ANTIBODIES TO CD40  
;; FILE REFERENCE: ABX-PF/3 US  
;; CURRENT APPLICATION NUMBER: US/11/211,917  
;; CURRENT FILING DATE: 2005-08-25  
;; PRIOR APPLICATION NUMBER: US/10/292,088  
;; PRIOR FILING DATE: 2002-11-08  
;; PRIOR APPLICATION NUMBER: 60/348,980  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 66  
;; LENGTH: 121  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-211-917-66

Query Match 76.4%; Score 465.5; DB 7; Length 121;  
Best Local Similarity 77.1%; Pred. No. 1.4e-36;  
Matches 91; Conservative 9; Mismatches 11; Indels 7; Gaps 2;

QY 2 ESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 61  
DB 6 ESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 63  
QY 62 KSRVTISVDTSKQFSLKLSNVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 114  
DB 64 KSRVTISVDTSKQFSLKLSNVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 121

RESULT 11  
US-10-994-679-68  
;; Sequence 68, Application US/10994679  
;; Publication No. US2006011559A2  
;; GENERAL INFORMATION:  
;; APPLICANT: Rososche, Viktor  
;; APPLICANT: Rosen, Craig A.  
;; APPLICANT: Ruben, Steven, M.  
;; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10  
;; FILE REFERENCE: 1488.1150001

;; CURRENT APPLICATION NUMBER: US/10/994,679  
;; CURRENT FILING DATE: 2004-11-23  
;; PRIOR APPLICATION NUMBER: US/10/067,800  
;; PRIOR FILING DATE: 2002-02-08  
;; PRIOR APPLICATION NUMBER: PCT/US01/04153  
;; PRIOR FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 09/779,880  
;; PRIOR FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 60/297,257  
;; PRIOR FILING DATE: 2001-06-12  
;; PRIOR APPLICATION NUMBER: 60/310,458  
;; PRIOR FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: 60/328,447  
;; PRIOR FILING DATE: 2001-10-12  
;; PRIOR APPLICATION NUMBER: 60/341,725  
;; PRIOR FILING DATE: 2001-12-21  
;; NUMBER OF SEQ ID NOS: 70  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 68  
;; LENGTH: 126  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-994-679-68

Query Match 76.0%; Score 463; DB 6; Length 126;  
Best Local Similarity 72.6%; Pred. No. 2.5e-36;  
Matches 90; Conservative 15; Mismatches 7; Indels 12; Gaps 3;

QY 1 LESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 60  
DB 5 VESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 62  
QY 61 LKSRVTISVDTSKQFSLKLSNVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 110  
DB 63 LKSRVTISVDTSKQFSLKLSNVTADTAIVYCARLDGYTLDI-----WGQGLTVTVSS 122  
QY 111 TVSS 114  
DB 123 TVSS 126

RESULT 12  
US-11-211-917-82  
;; Sequence 82, Application US/11211917  
;; Publication No. US2006093600A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BEDIAN, VAHE  
;; APPLICANT: GLADUE, RONALD P.  
;; APPLICANT: CORVALAN, JOSE  
;; APPLICANT: JIA, XIAO-CHI  
;; APPLICANT: FENG, XIAO  
;; TITLE OF INVENTION: ANTIBODIES TO CD40  
;; FILE REFERENCE: ABX-PF/3 US  
;; CURRENT APPLICATION NUMBER: US/11/211,917  
;; CURRENT FILING DATE: 2005-08-25  
;; PRIOR APPLICATION NUMBER: US/10/292,088  
;; PRIOR FILING DATE: 2002-11-08  
;; PRIOR APPLICATION NUMBER: 60/348,980  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 82  
;; LENGTH: 121  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-11-211-917-82

Query Match 75.9%; Score 462.5; DB 7; Length 121;  
Best Local Similarity 76.3%; Pred. No. 2.7e-36;  
Matches 90; Conservative 11; Mismatches 10; Indels 7; Gaps 2;

QY 2 ESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 61  
DB 25 ESGPGLVKAQTLISLCAVSGSIRSGGYWWSWIRHPGKLEWIGIYHSNTYNSPL 82



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GenCore version 5.1.9  
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# OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 102.427 Seconds  
(without alignments)  
508.875 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LBSGPGVLRPSQTLSTLCTV.....RSDPYTLDMWGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapext 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	605	98.5	114	5	ABG30447 Human IGE
2	600	97.7	114	5	ABG30446 Human IGE
3	586	90.6	114	5	ABG30445 Human IGE
4	532.5	86.7	121	10	Aef171064 H1gh freq
5	524.5	85.4	121	7	ADP03982 Murine-ex
6	524	85.3	118	7	ADP03968 Murine-ex
7	523.5	85.3	123	7	ADP03870 Murine-ex
8	521	84.9	120	7	ADP03974 Murine-ex
9	521	84.9	120	7	ADP03873 Murine-ex
10	521	84.9	122	7	ADP03977 Murine-ex
11	521	84.9	473	4	AAB36206 Human imm
12	519.5	84.6	121	7	ADJ32126 Human int
13	519.5	84.6	121	7	ADP03981 Murine-ex
14	519.5	84.6	125	7	ADP03871 Murine-ex
15	517.5	84.3	119	7	ADP03970 Murine-ex
16	517.5	84.3	148	10	AEB34855 Antibody
17	517.5	84.3	148	10	AEB34853 Antibody
18	516.5	84.1	123	2	AAW78433 Antibody
19	516.5	84.1	123	5	ABB97976 Heavy cha
20	516.5	84.1	123	7	ADG8414 Anti-Ob-R
21	516.5	84.1	123	7	ADP03872 Murine-ex
22	516.5	84.1	144	9	ADX98263 Human ant
23	516	84.0	124	7	ADP03935 Murine-ex

## ALIGNMENTS

24	515.5	84.0	117	7	ADC99784	Adc99784 Anti-huma
25	515.5	84.0	117	7	ADDO5388	AdDO5388 Anti-MUC1
26	515.5	84.0	117	7	ADFO9826	AdFO9826 Human ant
27	515	83.9	125	8	ADSI6556	AdSI6556 Human ant
28	514	83.7	120	7	ADP03958	AdP03958 Murine-ex
29	514	83.7	120	7	ADP03969	AdP03969 Murine-ex
30	514	83.7	121	7	ADJ80377	AdJ80377 Antibody
31	514	83.7	121	8	ADSI6559	AdSI6559 Human ant
32	514	83.7	122	9	AEA21492	Aea21492 Human ant
33	513.5	83.6	120	4	AAB62775	Aab62775 Human HIV
34	513	83.6	116	7	ADP03957	AdP03957 Murine-ex
35	512.5	83.5	125	7	ADP03868	AdP03868 Murine-ex
36	512.5	83.5	125	7	ADP03876	AdP03876 Murine-ex
37	512.5	83.5	480	9	ADZ57697	AdZ57697 Anti-CMet
38	512	83.4	123	4	AA862745	Aab62745 Human HIV
39	511.5	83.3	119	7	ADP03961	AdP03961 Murine-ex
40	511.5	83.3	140	9	ADX98269	AdX98269 Human ant
41	511	83.2	110	7	ADP03934	AdP03934 Murine-ex
42	510.5	83.1	122	4	AAB62765	Aab62765 Human HIV
43	510.5	83.1	123	7	ADP03869	AdP03869 Murine-ex
44	510.5	83.1	127	7	ADP03874	AdP03874 Murine-ex
45	510.5	83.1	148	9	ADX98259	AdX98259 Human ant

RESULT 1  
ABG30447  
ID ABG30447 standard; protein; 114 AA.

XX ABG30447;

DT 21-OCT-2002 (first entry)

DE Human IGE Fab clone 100 heavy chain protein.

KW Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;

KM timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..26

FT Region /note= "FR1 region"

FT Region /note= "CDR1 region"

FT Region /note= "FR2 region"

FT Region /note= "CDR2 protein"

FT Region /note= "FR3 region"

FT Region /note= "CDR2 region"

FT Region /note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-0004892.

XX (PHAA ) PHARMACIA DIAGNOSTICS AB.

XX Flicker's, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX DR N-PSDB; ABR9639.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.  
 XX  
 XX  
 PS Disclosure; Page 38; 45pp; English.  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific Fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The Fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific Fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC Fab, clone 100 heavy chain protein of the invention  
 CC  
 XX Sequence 114 AA;  
 SQ  
 Query Match 98.5%; Score 605; DB 5; Length 114;  
 Best Local Similarity 99.1%; Pred. No. 4.1e-44;  
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLSTLCYVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSGNTYVNS 60  
 DB 1 LESGPGLVKPSQTLSTLCYVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSGNTYVNS 60  
 QY 61 LKSRVTMSVDTSKNPSRLTSSVTADTAIVYYCARSDGYTLDMWGQGTLYTVSS 114  
 DB 61 LKSRVTMSVDTSKNPSRLTSSVTADTAIVYYCARSDGYTLDMWGQGTLYTVSS 114  
 RESULT 2  
 ABG30446  
 ID ABG30446 standard; protein; 114 AA.  
 AC ABG30446;  
 XX  
 XX 21-OCT-2002 (first entry)  
 DT  
 XX Human IgE Fab clone 60 heavy chain protein.  
 DE  
 XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 KM timothy grass pollen allergen; passive immunotherapy.  
 KM  
 XX Homo sapiens.  
 OS  
 XX  
 XX Location/Qualifiers  
 FH 1..26  
 FT Region /note= "FR1 region"  
 FT 27..33  
 FT Region /note= "CDR1 region"  
 FT 34..47  
 FT Region /note= "FR2 region"  
 FT 48..63  
 FT Region /note= "CDR2 protein"  
 FT 64..95  
 FT Region /note= "FR3 region"  
 FT 96..103  
 FT Region /note= "CDR2 region"  
 FT 104..114  
 FT Region /note= "FR4 region"  
 FT  
 XX W0200253595-A1.  
 XX  
 XX 11-JUL-2002.  
 XX

PF 27-DEC-2001; 2001WO-SB002908.  
 XX  
 XX 29-DEC-2000; 2000SE-00004892.  
 PR  
 XX (PHAA ) PHARMACIA DIAGNOSTICS AB.  
 PA  
 XX Flicker S, Steinberger P, Kraft D, Valenta R;  
 PI  
 XX WPI: 2002-563604/62.  
 DR N-PSDB; ABK9638.  
 XX  
 XX Group 2 allergen-specific immunoglobuline (Ig) E Fabs or IgG comprising  
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
 PT diagnosing or passive immunotherapy of type I allergy, for environmental  
 PT allergen detection.  
 XX  
 XX  
 PS Disclosure; Page 37; 45pp; English.  
 CC This invention relates to the DNA and protein sequences of group 2  
 CC allergen-specific human IgE Fabs and methods for their use. The proteins  
 CC of the invention may have antiallergic activities and may be used as a  
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
 CC 2 allergen-specific Fabs of the invention may be useful for environmental  
 CC allergen detection and for standardisation of allergen extracts. The Fabs  
 CC - or a vaccine against a type I allergy is useful for passive  
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
 CC I allergy. The allergen-specific Fabs of the invention are useful for  
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
 CC also useful for identification of group 2 allergen-containing pollen and  
 CC may be used for blocking the binding of grass pollen allergic patients  
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG  
 CC Fab, clone 60 heavy chain protein of the invention  
 CC  
 XX Sequence 114 AA;  
 SQ  
 Query Match 97.7%; Score 600; DB 5; Length 114;  
 Best Local Similarity 96.5%; Pred. No. 1.1e-43;  
 Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LESGPGLVKPSQTLSTLCYVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSGNTYVNS 60  
 DB 1 LESGPGLVKPSQTLSTLCYVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSGNTYVNS 60  
 QY 61 LKSRVTMSVDTSKNPSRLTSSVTADTAIVYYCARSDGYTLDMWGQGTLYTVSS 114  
 DB 61 LKSRVTMSVDTSKNPSRLTSSVTADTAIVYYCARSDGYTLDMWGQGTLYTVSS 114  
 RESULT 3  
 ABG30445  
 ID ABG30445 standard; protein; 114 AA.  
 AC ABG30445;  
 XX  
 XX 21-OCT-2002 (first entry)  
 DT  
 XX Human IgE Fab clone 94 heavy chain protein.  
 DE  
 XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;  
 KM timothy grass pollen allergen; passive immunotherapy.  
 KM  
 XX Homo sapiens.  
 OS  
 XX  
 XX Location/Qualifiers  
 FH 1..26  
 FT Region /note= "FR1 region"  
 FT 27..33  
 FT Region /note= "CDR1 region"  
 FT 34..47  
 FT Region /note= "FR2 region"  
 FT 48..63  
 FT Region /note= "CDR2 protein"  
 FT



ADP03982  
 ID ADP03982 standard; protein; 121 AA.  
 XX  
 AC ADP03982;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.  
 XX  
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KM cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KM cervical intraepithelial squamous neoplasia;  
 KM cervical intraepithelial glandular neoplasia;  
 KM gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 PN MO2003048328-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002MO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudus J, Foltz I, Handa M, Gallo M;  
 XX  
 DR WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Example 2; SEQ ID NO 152; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosolic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX  
 SQ Sequence 121 AA;  
 XX  
 Query Match 85.4%; Score 524.5; DB 7; Length 121;  
 Best Local Similarity 86.2%; Pred. No. 3.3e-37;  
 Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;  
 QY 2 ESGGGLVPSQTLSTCTVSGSGSIRGGYWSWIRPGKLEWIGYIYHSGNTYNNPSL 61  
 DB 6 ESGGGLVPSQTLSTCTVSGSGSIRGGYWSWIRPGKLEWIGYIYHSGNTYNNPSL 65  
 QY 62 KSRVTMSVDSKKNHPSLRLSSVTAAADTAVYYCARSD--GYTLDMNGGGLVTVSS 114  
 DB 66 KSRVTISVDSKKNQPSLKLSSVTAAADTAVYYCAYYDILTGAFDILWGGTMTVTVSS 121  
 XX  
 RESULT 6  
 ADP03968  
 ID ADP03968 standard; protein; 118 AA.  
 XX  
 AC ADP03968;  
 XX  
 DT 29-JUL-2004 (first entry)

XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.  
 XX  
 KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KM cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KM cervical intraepithelial squamous neoplasia;  
 KM cervical intraepithelial glandular neoplasia;  
 KM gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 PN MO2003048328-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002MO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudus J, Foltz I, Handa M, Gallo M;  
 XX  
 DR WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Example 2; SEQ ID NO 138; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mAb)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosolic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 XX  
 SQ Sequence 118 AA;  
 XX  
 Query Match 85.3%; Score 524; DB 7; Length 118;  
 Best Local Similarity 88.5%; Pred. No. 3.6e-37;  
 Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
 QY 2 ESGGGLVPSQTLSTCTVSGSGSIRGGYWSWIRPGKLEWIGYIYHSGNTYNNPSL 61  
 DB 6 ESGGGLVPSQTLSTCTVSGSGSIRGGYWSWIRPGKLEWIGYIYHSGNTYNNPSL 65  
 QY 62 KSRVTMSVDSKKNHPSLRLSSVTAAADTAVYYCARSDGYTLDMNGGGLVTVSS 114  
 DB 66 KSRVTISVDSKKNQPSLKLSSVTAAADTAVYYCARYYGGSDYVGGGLTVTVSS 118  
 XX  
 RESULT 7  
 ADP03870  
 ID ADP03870 standard; protein; 123 AA.  
 XX  
 AC ADP03870;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.  
 XX  
 KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KM cytosolic; colorectal neoplasm; renal cell carcinoma;  
 KM cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 XX gene therapy; murine; mouse; human; heavy chain variable domain.  
 OS Unidentified.  
 XX  
 XX PN - WO2003048328-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudae J, Foltz I, Handa M, Gallo M;  
 XX  
 DR WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Claim 1; SEQ ID NO 10; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosstatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 CC  
 SQ Sequence 123 AA;  
 Query Match 85.3%; Score 523.5; DB 7; Length 123;  
 Best Local Similarity 85.6%; Pred. No. 4.1e-37;  
 Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;  
 QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYWSWIRPQPGKLEWIGIYHSGNTYNP SL 61  
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYYWSWIRPQPGKLEWIGIYHSGNTYNP SL 65  
 QY 62 KSRVTSVDTSKNHFSLRLSSVTAADTAAYVCARS-----DGYTLDMWGQGLVTYVSS 114  
 DB 66 KSRVTSVDTSKNHFSLRLSSVTAADTAAYVCARAGKRYSGSYLDYMGQGLVTYVSS 123

RESULT 8  
 ADP03974  
 ID ADP03974 standard; protein; 120 AA.  
 AC ADP03974;  
 DT 29-JUL-2004 (first entry)  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.  
 XX  
 XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 XX PN WO2003048328-A2.

XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudae J, Foltz I, Handa M, Gallo M;  
 XX  
 DR WPI; 2003-523295/49.  
 XX  
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,  
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical  
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.  
 XX  
 PS Example 2; SEQ ID NO 144; 89pp; English.  
 XX  
 CC The invention relates to a novel isolated monoclonal antibody (mab)  
 CC comprising a heavy chain polypeptide and light chain polypeptide having a  
 CC sequence chosen from one of 53 fully defined amino acid sequences given  
 CC in the specification, where the antibody specifically binds carbonic  
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention  
 CC demonstrates cytosstatic activity and may be useful for treating a tumour,  
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,  
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal  
 CC tumour or breast cancer, possibly via gene therapy. The current sequence  
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH  
 CC (heavy chain variable domain) protein of the invention. The protein was  
 CC generated via the introduction of the human CA IX protein into a  
 CC transgenic mouse strain.  
 CC  
 CC  
 SQ Sequence 120 AA;  
 Query Match 84.9%; Score 521; DB 7; Length 120;  
 Best Local Similarity 87.1%; Pred. No. 6.6e-37;  
 Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;  
 QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYWSWIRPQPGKLEWIGIYHSGNTYNP SL 61  
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYYWSWIRPQPGKLEWIGIYHSGNTYNP SL 65  
 QY 62 KSRVTSVDTSKNHFSLRLSSVTAADTAAYVCARSQGYT---LDNMWGQGLVTYVSS 114  
 DB 66 KSRVTSVDTSKNHFSLRLSSVTAADTAAYVCAR-DGYNTYTDLMGRGLVTYVSS 120

RESULT 9  
 ADP03873  
 ID ADP03873 standard; protein; 120 AA.  
 AC ADP03873;  
 DT 29-JUL-2004 (first entry)  
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.  
 XX  
 XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;  
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;  
 KW cervical intraepithelial squamous neoplasia;  
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;  
 KW gene therapy; murine; mouse; human; heavy chain variable domain.  
 XX  
 OS Unidentified.  
 XX  
 XX PN WO2003048328-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038550.  
 XX  
 PR 03-DEC-2001; 2001US-0337275P.

```

XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M,
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 13; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytosolic-activity and may be useful for treating a tumor,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 120 AA;
XX
Query Match 84.9%; Score 521; DB 7; Length 120;
Best Local Similarity 87.1%; Pred. No. 6.6e-37;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
XX
QY 2 ESGGGLVKKPSQTLSTCTVSGGSIKSGGYWMIKRPKGKLEWIGYIHSGNTYNPSTL 61
DB 6 ESGGGLVKKPSQTLSTCTVSGGSIKSGGYWMIKRPKGKLEWIGYIHSGNTYNPSTL 65
XX
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR--SDGYTLDMNGGTLTVYSS 114
DB 66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCAR-DEINWYFDMRGTLTVYSS 120
XX
RESULT 10
ADP03977 ID ADP03977 standard; protein; 122 AA.
XX
AC ADP03977;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytosolic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PP 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M,
XX
DR WPI; 2003-523295/49.

```

```

XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Example 2; SEQ ID NO 147; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytosolic activity and may be useful for treating a tumor,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 122 AA;
XX
Query Match 84.9%; Score 521; DB 7; Length 122;
Best Local Similarity 85.5%; Pred. No. 6.7e-37;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
XX
QY 2 ESGGGLVKKPSQTLSTCTVSGGSIKSGGYWMIKRPKGKLEWIGYIHSGNTYNPSTL 61
DB 6 ESGGGLVKKPSQTLSTCTVSGGSIKSGGYWMIKRPKGKLEWIGYIHSGNTYNPSTL 65
XX
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR--SDGYTLDMNGGTLTVYSS 114
DB 66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARVYDILTGQMDWGGGTLTVYSS 122
XX
RESULT 11
AAB36206 ID AAB36206 standard; protein; 473 AA.
XX
AC AAB36206;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISP-4.
XX
KW Human; immune system associated protein; HISP-4; immune disorder;
KW infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PP 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lai P, Corley NC, Guejler KU, Baughn MR;
PI Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
XX
DR N-PSDB; AAC65522.
XX
PT New human immune system associated proteins (HISP) and polynucleotides
PT encoding the HISP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
PS Claim 1; Col 53-56; 54pp; English.

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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 / Search time 10.7091 Seconds  
(without alignments)  
1024.243 Million cell updates/sec

Title: US-10-027-725a-9

Perfect score: 614

Sequence: 1 BSGPGLVKPSQTLSTLCTV.....RSDGYTLDMWGGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:80:\*\n2: PIR:1:\*\n3: PIR:3:\*\n4: PIR:4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501.5	81.7	135	2 S78051	Ig heavy chain pre
2	497.5	81.0	147	2 S13559	Ig heavy chain V r
3	492.5	80.2	140	2 I37782	Ig variable region
4	490	79.8	130	2 S30534	Ig heavy chain V r
5	488.5	79.6	116	2 S37456	Ig mu chain - huma
6	487.5	79.4	130	2 S31690	Ig heavy chain V r
7	480.5	78.3	121	2 S44113	Ig heavy chain V r
8	479.5	78.1	155	2 S31511	Ig heavy chain - h
9	477.5	77.8	146	2 S09710	Ig heavy chain V r
10	477.5	77.8	155	2 S31512	Ig heavy chain - h
11	473.5	77.1	146	2 S09711	Ig heavy chain V r
12	472.5	77.0	127	2 S19668	Ig heavy chain V r
13	472.5	77.0	128	2 S31514	Ig heavy chain - h
14	472	76.9	137	2 S31676	Ig heavy chain V r
15	469	76.4	99	2 S26803	Ig heavy chain V r
16	467.5	76.1	123	2 S30530	Ig heavy chain V r
17	467	76.1	99	2 S26801	Ig heavy chain V r
18	467	76.1	122	2 S69912	Ig V-D-J region (N
19	465	75.7	139	2 S31586	Ig heavy chain V r
20	464	75.6	99	2 S26802	Ig heavy chain V r
21	461	75.1	145	2 S78055	Ig heavy chain pre
22	460.5	75.0	109	2 PH1673	Ig heavy chain V r
23	459	74.8	110	2 S44110	Ig heavy chain V-D
24	458	74.6	139	2 A41212	Ig heavy chain pre
25	457	74.4	118	2 A26340	Ig heavy chain V-I
26	454	73.9	97	2 PL0118	Ig heavy chain V r
27	454	73.9	99	2 S26839	Ig heavy chain V r
28	452	73.6	135	2 S31604	Ig heavy chain V r
29	451	73.5	118	2 S20780	Ig heavy chain V r

30	451	73.5	129	2 S44114	Ig heavy chain V r
31	448	73.0	99	2 S12418	Ig heavy chain V r
32	447.5	72.9	139	2 S31696	Ig heavy chain V r
33	445.5	72.6	137	2 S31585	Ig heavy chain V r
34	445.5	72.6	140	2 A49045	Ig heavy chain V r
35	445	72.5	120	2 PT0370	Ig mu chain precu
36	444	72.3	126	2 S47010	Ig heavy chain V4.
37	443	72.1	99	2 S26800	Ig heavy chain V r
38	442	72.0	105	2 S44125	Ig lambda chain V
39	442	72.0	105	2 S44125	Ig lambda chain V
40	442	72.0	118	2 S24443	Ig heavy chain V r
41	442	72.0	140	2 S78052	Ig heavy chain pre
42	441.5	71.9	98	2 S12421	Ig heavy chain V r
43	441.5	71.9	132	2 A38911	Ig heavy chain V r
44	441.5	71.9	140	2 A24770	hypothetical hybr
45	441	71.8	97	2 S26906	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_rev15ion 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051, S23716

R/Harindranath, N.  
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 &lt;HAR&gt;

A/Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:g37814; PIDN:CA38306.1; PID:R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Butastero, S.B.; Wilder, R.L.; Nockins, Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity B cell receptors.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A/Molecule type: mRNA

A/Residues: 13-111 &lt;HAW&gt;

A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_rev15ion 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051, S23716

R/Harindranath, N.  
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_rev15ion 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051, S23716

R/Harindranath, N.  
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_rev15ion 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051, S23716

R/Harindranath, N.  
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1997 #sequence\_rev15ion 05-Dec-1997 #text\_change 23-Jul-1999

C/Accession: S78051, S23716

R/Harindranath, N.  
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

## RESULT 2

Ig heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 25-Feb-1994 #sequence\_rev15ion 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S13519  
R/Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A/Reference number: S13519; MUID:9187691; PMID:2011536  
A/Accession: S13519

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <MOR>  
A:Cross-references: UNIPARC:UP10000115EB5; EMBL:X56158; NID:937724; PIDN:CAA39626.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;  
Best Local Similarity 82.8%; Pred. No. 7e-38;  
Matches 96; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

Oy 2 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 61  
Db 32 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 91

Oy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG---GYTLDMWGQGLTVTVSS 114  
Db 92 KSRVTISVDTSKNHFSLRLSSVTADTAIVYVCARPLMFGELFDYWGQGLTVTVSS 147

## RESULT 3

I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A:Title: Somatic diversification in the heavy chain variable region genes expressed by h  
A:Reference number: A36876; MUID:9411917; PMID:8290556  
A:Accession: I37782

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: UNIPARC:UP10000176E83; EMBL:X67906; NID:933562; PIDN:CAA48104.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:46-126/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 492.5; DB 2; Length 140;  
Best Local Similarity 82.2%; Pred. No. 1.9e-37;  
Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

Oy 2 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 61  
Db 25 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 82

Oy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG---GYTLDMWGQGLTVTVSS 114  
Db 83 KSRVTISVDTSKNHFSLRLSSVTADTAIVYVCARHSSSMYGRYFDYWGQGLTVTVSS 140

## RESULT 4

S30534  
Ig heavy chain V region - human

C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C:Accession: S30534  
R:Marlette, X.  
submitted to the EMBL Data Library, October 1992

A:Reference number: S30520  
A:Accession: S30534  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <MAR>  
A:Cross-references: UNIPARC:UP10000113F45; EMBL:Z18320  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 490; DB 2; Length 130;  
Best Local Similarity 78.4%; Pred. No. 2.9e-37;  
Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

Oy 2 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 61  
Db 6 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 65

Oy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG---GYTLDMWGQGLTVTVSS 114  
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAIVYVCARHSSSMYGRYFDYWGQGLTVTVSS 125

Oy 110 VTVSS 114  
Db 126 VTVSS 130

## RESULT 5

S37456  
Ig mu chain - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S37456  
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.  
submitted to the EMBL Data Library, September 1993

A:Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from f  
A:Reference number: S37453  
A:Accession: S37456  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <MCI>  
A:Cross-references: UNIPARC:UP100001161C0; EMBL:X75024; NID:9404313; PIDN:CAA52932.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:6-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 488.5; DB 2; Length 116;  
Best Local Similarity 81.2%; Pred. No. 3.5e-37;  
Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

Oy 6 GLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 65  
Db 1 GLVPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 60

Oy 66 TMSVDTSKNHFSLRLSSVTADTAIVYVCARSDG---LDNMGQGLTVTVSS 114  
Db 61 TISVDTSKNHFSLRLSSVTADTAIVYVCARG-GYSYGYYYVYDWMGKGLTVTVSS 116

## RESULT 6

S31690  
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31690  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the f  
A:Reference number: S31585  
A:Accession: S31690  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-130 <CUI>  
A:Cross-references: UNIPARC:UP10000116471; EMBL:Z14199; NID:930984; PIDN:CAA78568.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:20-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 130;  
Best Local Similarity 78.7%; Pred. No. 4.8e-37;  
Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

Oy 2 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 61  
Db 11 ESGGGLVLPKPSQTLSTCTVSGGSIIRSGGYWMIROPKGLKLEWIGYIYHSGNTYVNSL 68

C/Species: Homo sapiens (man)  
C/Date: 21-NOV-1993 #seemance revision 10-NOV-1995 #text change 16-AUG-1996

C/Accession: S09711  
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A/Reference number: S09710; MUID:90262535; PMID:2111699  
A/Accession: S09711  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-146 <HUG>  
A/Cross-references: UNIPARC:UPI0000176CD3  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;  
Best Local Similarity 73.8%; Pred. No. 1e-35;  
Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61  
DB 25 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 84  
QY 62 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCAR-----SDGYTLDNMGQGLTVTV 112  
DB 85 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCARVLVSRISQSYMDVWGKGTIVTV 144  
QY 113 SS 114  
DB 145 SS 146

## RESULT 12

S19668  
Ig heavy chain V region (VH4DJH6) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 20-Jun-2000  
C/Accession: S19668; S24445  
R/Marks: J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A/Title: Bypassing immunization. Human antibodies from V-gene libraries displayed on ph  
A/Reference number: S19663; MUID:92085276; PMID:1748994  
A/Accession: S19668  
A/Molecule type: mRNA  
A/Residues: 1-127 <MAR>  
A/Cross-references: UNIPARC:UPI0000176C7F; EMBL:X61648  
R/Jones, P.T.  
submitted to the EMBL Data Library, October 1991  
A/Reference number: S24442  
A/Accession: S24445  
A/Molecule type: mRNA  
A/Residues: 1-116, 'E', '120-121', 'T', '123-126', 'F' <JON>  
A/Cross-references: UNIPARC:UPI0000115FE7; EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;  
Best Local Similarity 74.6%; Pred. No. 1.1e-35;  
Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61  
DB 6 QSGGGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 65  
QY 62 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCARSDG-----YTLDNMGQGLTVTV 112  
DB 66 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCARSDG-----YTLDNMGQGLTVTV 125  
QY 113 SS 114  
DB 126 SS 127

## RESULT 13

S31514  
Ig heavy chain - human

C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31514  
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoe  
A/Reference number: S31509  
A/Accession: S31514  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-128 <CHA>  
A/Cross-references: UNIPARC:UPI00001160FB; EMBL:X69862; NID:933086; PIDN:CAA49496.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;  
Best Local Similarity 78.4%; Pred. No. 1.1e-35;  
Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61  
DB 13 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 72  
QY 62 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCAR-----SDGYTLDNMGQGLTVTVSS 114  
DB 73 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCARIGVNGFGDPGQGLTVTVSS 128

## RESULT 14

S31676  
Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31676  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the f  
A/Reference number: S31585  
A/Accession: S31676  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-137 <CUI>  
A/Cross-references: UNIPARC:UPI0000116461; EMBL:Z14182; NID:931031; PIDN:CAA78551.1; PID  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;  
Best Local Similarity 82.6%; Pred. No. 1.3e-35;  
Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 61  
DB 25 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPPGKGLWIGIYHSGNTYNNPSL 82  
QY 62 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCARSDG-----YTLDNMGQGLTVTVSS 114  
DB 83 KSRVTMSVDTSKQHFSLRLSSVTADPAVYVCARSDG-----YTLDNMGQGLTVTVSS 137

## RESULT 15

S26803  
Ig heavy chain V region - human

C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S26803  
R/Meng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.  
Eur. J. Immunol. 22, 1075-1082, 1992  
A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.

A:Reference number: S26800; MUID:92201299; PMID:1348029  
A:Accession: S26803  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <WEN>  
A:Cross-references: UNIPARC:UP00000116485; EMBL:Z14238; NID:g37710; PIDD:CAA78607.1; PIRIT:PIR00000116485  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
E15-99/Domain: immunoglobulin homology <IMM>

Query Match	76.4%;	Score 469;	DB 2;	Length 99;
Best Local Similarity	92.6%;	Pred. No. 1.7e-35;		
Matches 87; Conservative	4;	Mismatches 3;	Indels 0;	Gaps 0;

```
QY      2 ESGPGLVKPSQLTSLTCVSSGGSIRGGIYWMSWLRQPCKGLEWCIIYHSNGNTYYNPSL    61  
       |||||  
Db      6 ESGPGLVKPSQLTSLTCVSSGGSISSDGYWSWI R QPKGLEWCIIYYSGSTYYNP SL   65
```

```
QY      62 KSRVTMSVDTSKNHFSRLSSVTADTAIVYYCAR 95
      ||||:||||| |||:|||||
Db      66 KSRVTISVDTSKNQFSKLSSVTADTAIVYYCAR 99
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Search completed: August 30, 2006, 00:42:54  
Job time : 11.7091 secs

5

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GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 62.1818 Seconds  
(without alignments)  
1695.862 Million cell updates/sec

Title: US-10-027-725A-9  
Perfect score: 614  
Sequence: 1 LBSGPGLVKPSQTLSTLCTV.....RSDGYTLDMWGQGLTVTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 2849598 segs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : UniProt 7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504.5	82.2	476	2	06GMX1_HUMAN
2	480	78.2	465	2	06GMX6_HUMAN
3	480	78.2	478	2	Q7Z379_HUMAN
4	470.5	76.6	119	2	Q9UL73_HUMAN
5	469.5	76.5	492	2	Q7Z374_HUMAN
6	469	76.4	477	2	06GMX7_HUMAN
7	468	76.2	150	2	Q95973_HUMAN
8	460	74.9	496	2	096KX8_HUMAN
9	460	74.9	620	2	096KX8_HUMAN
10	452	73.6	576	2	Q6P418_HUMAN
11	441	71.8	139	2	086SX2_HUMAN
12	439.5	71.6	129	1	HV2F_HUMAN
13	431	70.2	130	2	081ZD7_HUMAN
14	429.5	70.0	595	2	08MTX4_HUMAN
15	429.5	70.0	597	2	06GMX5_HUMAN
16	429.5	70.0	597	2	Q9BU10_HUMAN
17	429.5	70.0	625	2	Q96AA6_HUMAN
18	425.5	69.3	597	2	Q9BOB8_HUMAN
19	424.5	69.1	478	2	Q6NYH3_HUMAN
20	420	68.4	146	1	HV2I_HUMAN
21	412	67.1	473	2	08TC63_HUMAN
22	393.5	64.1	117	1	HV2G_HUMAN
23	393	64.0	483	2	Q5U413_MOUSE
24	392.5	63.9	479	2	Q99M22_MOUSE
25	389	63.4	116	2	Q7Z376_HUMAN
26	387	63.0	136	2	Q6LBD5_MOUSE
27	377.5	61.5	476	2	Q6MZ87_HUMAN
28	377.5	61.5	615	2	Q569B6_RAT
29	375.5	61.2	119	2	Q53VW3_MOUSE
30	372.5	60.7	137	1	HV46_MOUSE
31	370.5	60.3	262	2	Q65Z11_MOUSE

32	369.5	60.2	590	2	Q569B8_RAT	Q569B8_rattus norv
33	368.5	60.0	477	2	Q510J1_RAT	Q510J1_rattus norv
34	367.5	59.9	115	2	Q53VQ1_MOUSE	Q53VQ1_mus musculu
35	365.5	59.5	119	2	Q53VQ5_MOUSE	Q53VQ5_mus musculu
36	364	59.3	122	2	Q9UL75_HUMAN	Q9UL75_homo sapien
37	361	58.8	120	2	Q53VR7_MOUSE	Q53VR7_mus musculu
38	357.5	58.2	113	1	HV47_MOUSE	P01823_mus musculu
39	353.5	57.6	98	2	Q53VR2_MOUSE	Q53VR2_mus musculu
40	353.5	57.6	119	2	Q53VQ9_MOUSE	Q53VQ9_mus musculu
41	352	57.3	485	2	Q561M5_MOUSE	Q561M5_mus musculu
42	349.5	56.9	144	1	HV43_MOUSE	P01819_mus musculu
43	348.5	56.8	116	1	HV61_MOUSE	P18532_mus musculu
44	348	56.7	591	2	Q510L9_RAT	Q510L9_rattus norv
45	347	56.5	117	1	HV62_MOUSE	P18533_mus musculu

## ALIGNMENTS

RESULT 1  
06GMX1\_HUMAN PRELIMINARY; PRT; 476 AA.  
AC 06GMX1;  
DT 19-JUL-2004, integrated into UniProtKB/TREMBL.  
DT 19-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splice;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Raba S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smilins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splice;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonCommercial  
CC EMBL; BC073773; AAT73773.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-1ike.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGC1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 KM SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 82.2%; Score 504.5; DB 2; Length 476;  
 Best Local Similarity 76.6%; Pred. No. 1.3e-43;  
 Matches 95; Conservative 12; Mismatches 4; Indels 13; Gaps 2;

QY 2 ESGPGLVKSQTSLTCTVSGSGSIRSGGYWSNIRPPGKGLWIGYIYHSGNTYNNPSL 61  
 DB 25 ESGPGLVKSQTSLTCTVSGSGSIRSGGYWSNIRPPGKGLWIGYIYHSGNTYNNPSL 84  
 QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSGYTLTDNNGGTLTV 110  
 DB 85 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSGYTLTDNNGGTLTV 142  
 QY 111 TVSS 114  
 DB 143 TVSS 146

## RESULT 2

06GMX6\_HUMAN PRELIMINARY; PRT; 465 AA.  
 AC 06GMX6;  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 16.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RX [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins L.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uscii T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiteley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RL Strausberg R.;  
 CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; BC073766; AAH73766.1; mRNA.  
 DR InterPro; IPR003599; IG; 1.

DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013106; V-sec.  
 DR Pfam; PF07654; C1-sec; 3.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGC1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 KM SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 78.2%; Score 480; DB 2; Length 465;  
 Best Local Similarity 84.1%; Pred. No. 4.4e-41;  
 Matches 95; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

QY 2 ESGPGLVKSQTSLTCTVSGSGSIRSGGYWSNIRPPGKGLWIGYIYHSGNTYNNPSL 61  
 DB 25 ESGPGLVKSQTSLTCTVSGSGSIRSGGYWSNIRPPGKGLWIGYIYHSGNTYNNPSL 82  
 QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSGYTLTDNNGGTLTV 114  
 DB 83 KSRVTSVDTSKNHFSLRLSSVTADTAAYVYCARSGYTLTDNNGGTLTV 135

## RESULT 3

07Z379\_HUMAN PRELIMINARY; PRT; 478 AA.  
 AC 07Z379;  
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 15.  
 DE Hypothetical protein DKFP686K04218 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RX [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Human rectum tumor;  
 RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobio G., Han M., Wiemann S;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
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 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC EMBL; BX538066; CAD97996.1; mRNA.  
 DR HSP; P01820; 167J.  
 DR SMK; Q7Z379; 248-456.  
 DR Ensemble; ENSG00000130076; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013106; V-sec.  
 DR Pfam; PF07654; C1-sec; 2.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGC1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KM Hypothetical protein; Immunoglobulin domain; Repeat.  
 FT NON TRP 1  
 SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match 78.2%; Score 480; DB 2; Length 478;  
 Best Local Similarity 77.4%; Pred. No. 4.6e-41;



Matches 89; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSGSIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61  
DB 24 ESGPGLVKPSQTLSTLCTVSGSGSIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 83

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDGY--TLDNMGQTLVTYSS 114  
DB 84 ESRLLTISIDTSKNQFSLRLNLTAAADTAVYFCARGVGLGTAFIDWGQGLVTYVSS 138

RESULT 4  
Q9UL73 HUMAN PRELIMINARY; PRT; 119 AA.

AC Q9UL73  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DE 07-FEB-2006, entry version 23.  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
RA Young D.C.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=9207875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;  
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,  
RA Diamond B.,  
RT "Molecular characteristics of antibodies bearing an anti-DNA-  
RT associated idiootype."  
RT J. Exp. Med. 174:1639-1652(1991).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=90059975; PubMed=2511001;  
RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.,  
RT "The smaller human VH gene families display remarkably little  
RT polymorphism."  
RT EMBO J. 8:3741-3748(1989).  
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CC EMBL AF035041; AAD56277.1; -, mRNA.  
DR PIR; PH0876; PH0876.  
DR PIR; S12416; S12416.  
DR HSSP; P01820; IGTJ.  
DR SMR; Q9UL73; 2-119.  
DR Linkhub; Q9UL73;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR SMART; SM00409; IG\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
FT NON TER 1  
FT NON TER 119  
SQ SEQUENCE 119 AA; 13219 MW; 1BD88686420EAOBE CRC64;

Query Match 76.6%; Score 470.5; DB 2; Length 119;  
Best Local Similarity 79.3%; Pred. No. 9,4e-41;  
Matches 92; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSGSIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGSGSIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG--YTLNMGQTLVTYSS 114  
DB 64 KSRVTISVDRSKNQFSLRLNLTAAADTAVYFCARLSNMGPIYFDWGQGLVTYVSS 119

RESULT 5  
Q7Z374 HUMAN PRELIMINARY; PRT; 492 AA.

AC Q7Z374  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DE 07-FEB-2006, entry version 16.  
DE Hypothetical protein DKFZp686C02218 (Fragment).  
GN Name=DKFZp686C02218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Human rectum tumor;  
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amdt C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.,  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
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CC EMBL BX538077; CAD98001.1; -, mRNA.  
DR HSSP; P01820; IGTJ.  
DR SMR; Q7Z374; 262-470.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; IG\_1.  
DR SMART; SM00407; IGV; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein; Immunoglobulin domain; Repeat.  
FT NON TER 1  
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 76.5%; Score 469.5; DB 2; Length 492;  
Best Local Similarity 76.9%; Pred. No. 5.8e-40;  
Matches 90; Conservative 10; Mismatches 12; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSGSIRSGGYWMIROPPGKGLWIGIYHSGNTYNPSTL 61  
DB 37 ESGPGLVKPSQTLSTLCTVSGSVSNRNTYMGIRPPGKGLWIGIYHSGNTYNPSTL 96

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAR---SDGYTLNMGQGLVTYSS 114  
DB 97 KSRITIFVDTSKNHFSLRLTSLTAADTAVYVCRAHVEGPGW-FDPMGQGLVTYVSS 152

RESULT 6  
Q6GKK7 HUMAN PRELIMINARY; PRT; 477 AA.

AC Q6GKK7  
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2004, sequence version 1.  
DE 07-FEB-2006, entry version 16.  
DE Hypothetical protein.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN NCBI\_TaxID=9606;  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tomshiyki S., Carninci P., Pange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muthaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: BC073765; AAHT3765.1; -, mRNA.  
 DR SMR: Q6GMX7; 247-455.  
 DR Ensembl: ENSG00000130076; Homo sapiens.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07654; C1-set; 2.  
 DR SMART: SM00409; IG1; 1.  
 DR SMART: SM00407; IG1; 2.  
 DR SMART: SM00406; IG1; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KM Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;  
 Query Match 76.4%; Score 469; DB 2; Length 477;  
 Best Local Similarity 80.0%; Pred. No. 6.3e-40;  
 Matches 92; Conservative 6; Mismatches 13; Indels 4; Gaps 2;  
 QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYVMSWIRQPGKGLWIGIYHSGNTYVNSL 61  
 DB 25 ESGGLVPSQTLSTCTVSGGSIIRSGYVMSWIRQPGKGLWIGIYHSGNTYVNSL 82  
 QY 62 KSRVTVSDTSKNHPSLRSLSSVTADTAAYVCARSDG--YTLDMWGQGLTVVSS 114  
 DB 83 KSRVTVSDTSKNHPSLRSLSSVTADTAAYVCARSDG--YTLDMWGQGLTVVSS 137  
 RESULT 7  
 ID 095973 HUMAN PRELIMINARY; PRT; 150 AA.  
 AC 095973;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;

DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-1999, sequence version 1.  
 DT 07-FEB-2006, entry version 23.  
 DE V4 heavy chain variable region precursor (Fragment).  
 DE  
 GN Name=IgM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN NCBI\_TaxID=9606;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
 RT "Clonal proliferation of IGM secreting B cell in the synovium of  
 RT Rheumatoid arthritis patient with arthritis."  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92031262; PubMed=1718404;  
 RA Hardiman N., Goldfarb I.S., Ikematsu H., Burastero S.E.,  
 RA Wilder R.L., Norkin A.L., Casali P.;  
 RT "Complete sequence of the genes encoding the VH and VL regions of low-  
 RT and high-affinity monoclonal IgM and IgA1 rheumatoid factors produced  
 RT by CD5+ B cells from a rheumatoid arthritis patient."  
 RL Int. Immunol. 3:865-875(1991).  
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 CC -----  
 DR EMBL: AF103795; AAC79084.1; -, mRNA.  
 DR PIR: S31673; S31673.  
 DR PIR: S78056; S78056.  
 DR HSSP: P01820; 1G7J.  
 DR SMR: Q95973; 20-147.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR InterPro: IPR013106; V-set.  
 DR SMART: SM00409; IG1; 1.  
 DR SMART: SM00406; IG1; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin domain; Signal.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 >150 V4 heavy chain variable region.  
 FT NON TER 150 150  
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;  
 Query Match 76.2%; Score 468; DB 2; Length 150;  
 Best Local Similarity 78.8%; Pred. No. 2.2e-40;  
 Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;  
 QY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYVMSWIRQPGKGLWIGIYHSGNTYVNSL 61  
 DB 25 ESGGLVPSQTLSTCTVSGGSIIRSGYVMSWIRQPGKGLWIGIYHSGNTYVNSL 84  
 QY 62 KSRVTVSDTSKNHPSLRSLSSVTADTAAYVCARSDG--YTLDMWGQGLTVVSS 114  
 DB 85 KSRVTVSDTSKNHPSLRSLSSVTADTAAYVCARSDG--YTLDMWGQGLTVVSS 137  
 RESULT 8  
 ID 096KX8 HUMAN PRELIMINARY; PRT; 496 AA.  
 AC 096KX8;  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 1.  
 DE MGC27165 protein.  
 DE  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Lung;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: BC016369; AA016369.1; -, mRNA.  
 DR HSSP; P01876; 10W0.  
 DR SMR; Q96KX8; 266-474.  
 DR Ensemble; ENSG00000130076; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1ike.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07654; C1-set; 2.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGc1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_MHC; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKOWN 1.  
 SQ SEQUENCE 496 AA; 53392 MW; D346929849040D69 CRC64;  
 Query Match 74.9%; Score 460; DB 2; Length 496;  
 Best Local Similarity 75.0%; Pred. No. 5.7e-39;  
 Matches 90; Conservative 8; Mismatches 14; Indels 8; Gaps 2;  
 Oy 2 ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPGKGLWIGIYHSGNTYVPSL 61  
 Db 25 ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPGKGLWIGIYHSGNTYVPSL 84  
 Oy 62 KSRVTVSVDTSKNHFSLRLSVTAADTAAYVYCARSDGYT-----LDNWGGTLVTVSS 114  
 Db 85 KSRVTVSVDTSKNHFSLRLSVTAADTAAYVYCAR-HGYSSRGRTGAIIDYGGGTLVTVSS 143  
 RESULT 9  
 Q96EYO HUMAN PRELIMINARY; PRT; 620 AA.  
 AC Q96EYO;  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 2.  
 DT 07-FEB-2006, entry version 26.  
 DE IGHM protein.  
 GN Name=IGHM;

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91252286; PubMed=1904154;  
 RA Neale G.A., Kitchingman G.R.;  
 RT "RNA transcripts initiating within the human immunoglobulin mu heavy  
 RT chain enhancer region contain a non-translatable exon and are  
 RL extremely heterogeneous at the 5' end.";  
 CC Nucleic Acids Res. 19:2427-2433(1991).  
 CC -----  
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 CC -----  
 CC EMBL: BC011857; AA011857.2; -, mRNA.  
 DR PIR; S15590; S15590.  
 DR HSSP; P01820; 1G7J.  
 DR SMR; Q96EYO; 27-251.  
 DR Ensemble; ENSG00000130076; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1ike.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGc1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_MHC; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKOWN 3.  
 SQ SEQUENCE 620 AA; 60125 MW; 990A1AA468BF27B CRC64;  
 Query Match 74.9%; Score 460; DB 2; Length 620;  
 Best Local Similarity 80.5%; Pred. No. 7.3e-39;  
 Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps 3;  
 Oy 2 ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPGKGLWIGIYHSGNTYVPSL 61  
 Db 32 ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWSMIRPGKGLWIGIYHSGNTYVPSL 89

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGTLTIDN-----MGOGTLVTYVSS 114  
 DB 90 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCA-SQWELPTVGLFTMGOGTLVTYVSS 146

RESULT 10  
 Q6P418 HUMAN PRELIMINARY; PRT; 576 AA.  
 ID Q6P418\_HUMAN  
 AC Q6P418; 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 21-FEB-2006, entry version 20.  
 DE IGHG protein.  
 GN Name-IGHG;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,  
 RA Altschul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.V., Scheetz T.E.,  
 RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Paley J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL: BC063384; AAF63384.1; -; mRNA.  
 DR HSSP; P01820; 1A7N.  
 DR Ensembl; ENSG00000196122; Homo sapiens.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1-like.  
 DR InterPro; IPR003597; IG-CL.  
 DR InterPro; IPR003506; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013151; Immunoglobulin.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00407; IGH1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS0290; IG MHC; UNKNOWN 2.  
 SQ SEQUENCE 576 AA; 63364 MW; FBB97C949D720FIE CRC64;

Query Match 73.6%; Score 452; DB 2; Length 576;  
 Best Local Similarity 77.6%; Pred. No. 4.6e-38;  
 Matches 90; Conservative 6; Mismatches 16; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLTCTVSGGSIKSGGYWWSIRPPGKGLWIGIYHSGNTYVPSL 61  
 DB 32 ESGPGLVKPSQTLTCTVSGGSIKSGGYWWSIRPPGKGLWIGIYHSGNTYVPSL 90

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG---YTLDNMGOGTLVTYVSS 114  
 DB 91 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDGIDYVGMVGGOGTLVTYVSS 146

RESULT 11  
 Q66SX2 HUMAN PRELIMINARY; PRT; 139 AA.  
 ID Q66SX2\_HUMAN  
 AC Q66SX2;  
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of  
 DE Homo sapiens (human) (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=B cells;  
 RA Li W.B., Gruber C., Jessee J., Polayes D.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=B cells;  
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RL Genoscope;  
 CC Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 CC EMBL: BX248300; CAD62627.1; -; mRNA.  
 DR HSSP; P01820; 1G7J.  
 DR SMR; Q66SX2; 34-132.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR InterPro; IPR013106; V-set.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin domain.  
 FT NON TER  
 SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 71.8%; Score 441; DB 2; Length 139;  
 Best Local Similarity 89.4%; Pred. No. 1.3e-37;  
 Matches 84; Conservative 5; Mismatches 3; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLTCTVSGGSIKSGGYWWSIRPPGKGLWIGIYHSGNTYVPSL 61  
 DB 38 ESGPGLVKPSQTLTCTVSGGSIKSGGYWWSIRPPGKGLWIGIYHSGNTYVPSL 95

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR 95  
 DB 96 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR 129

RESULT 12  
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 AC P01824;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 07-MAR-2006, entry version 36.  
 DE Ig heavy chain V-II region WH4.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debutre B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma
CC protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
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CC
CC PIR: A02099; D2HUMA.
CC PDB: 1ZVO; X-ray; C/D=..
CC
DR SMR; P01824; 2-129.
DR Glycosylated; P01824; -.
DR GO; GO:0005576; Cellular region; NAS.
DR GO; GO:0003823; Antigen binding; NAS.
DR GO; GO:0006955; Immune response; NAS.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR Pfam; PF00686; V-set; 1.
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DR SMART; SM00406; IGV; 1.
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DR 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >129
FT Ig heavy chain V-II region WAH.
FT /FTID=PRO_0000059912.
FT DOMAIN 1 113
FT NON_TER 129 129 Ig-like.
FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;
SQ
Query Match 71.6%; Score 439.5; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 1,7e-37;
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWSMIROPPGKGLFWIGYIHSGNTYNSPL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWSMIROPPGKGLFWIGYIHSGNTYNSPL 65
QY 62 KSRVYMSVPTSKNHFSLRLSSVTAAADTAAYVYCAR-----SDGYTLDNMGGCT 108
DB 66 KSRVYMSVPTSKNHFSLRLSSVTAAADTAAYVYCAR-----SDGYTLDNMGGCT 123
QY 109 LVTVSS 114
DB 124 TVTVSS 129

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RP NUCLEOTIDE SEQUENCE.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
CC EMBL; AY145445; AAN64329.1; -; mRNA.
CC
DR HSSP; P01820; 1G7J.
DR SMR; O81ZD7; 1-130.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin domain.
FT CHAIN 1 130
FT NON_TER 130 130
FT SEQUENCE 130 AA; 13901 MW; 036131FC6ECL551E CRC64;
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Best Local Similarity 71.2%; Pred. No. 1,3e-36;
Matches 89; Conservative 8; Mismatches 16; Indels 12; Gaps 4;
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DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWSMIROPPGKGLFWIGYIHSGNTYNSPL 65
QY 57 YNPSLKRYTMSVDYTSKNHFSLSVTAADTAAYVYCAR-----SDG--YT-LDNMGQTL 109
DB 66 YNPSLKRYTMSVDYTSKNHFSLSVTAADTAAYVYCAR-----SDG--YT-LDNMGQTL 125
QY 110 VTVSS 114
DB 126 VTVSS 130

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RESULT 14
O8WDX4 HUMAN PRELIMINARY; PRT; 595 AA.
AC O8WDX4;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004, sequence version 2.
DT 07-FEB-2006, entry version 24.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marcusa K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

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RT "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RA Strauberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99235232; PubMed=2497188;  
 RA Sanz I., Casali P., Thomas J.W., Nocking A.L., Capra J.D.;  
 RT "Nucleotide sequences of eight human natural autoantibody VH regions  
 RT reveals apparent restricted use of VH families.";  
 RL J. Immunol. 142:4054-4061(1989).  
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 CC -----  
 DR EMBL: BC019235; AAH19235.2; -, mRNA.  
 DR PIR: G34964; G34964.  
 DR HSP: P01861; IADQ.  
 DR SMR: Q8WUX4; 27-256.  
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 DR InterPro: IPR003599; IG.  
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 DR InterPro: IPR003597; IG\_c1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07654; C1-set; 4.  
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 DR SMART: SM00406; IGv; 1.  
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 KM Hypothetical protein.  
 SQ SEQUENCE 595 AA; 65291 MW; 004B5076545714E CRC64;  
 Query Match 70.0%; Score 429.5; DB 2; Length 595;  
 Best Local Similarity 72.5%; Pred. No. 1e-35;  
 Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;  
 QY 4 GPGLVKPSQTLSTCTVSGSIRSGYWSWIRPPGKGLGEMWIGYHSGNTYVNSLKS 63  
 DB 34 GAGILKPSERTSLTCGVYGSF--SGYWSWIRPPGKGLGEMWIGYHSGNTYVNSLKS 91  
 QY 64 RVTISVDTSKNHFSLRLSSVTADTAVYYCAR-----SDG-YTLDMWGQGLTVVSS 114  
 DB 92 RVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMQVWGQGLTVVSS 151  
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 AC Q6GMX5;  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 17.  
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 GN Name=IGHM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NC NCBI\_TaxID=9606;  
 CC [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millay S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
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 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lymph;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: BC073767; AAH73767.1; -, mRNA.  
 DR SMR: Q6GMX5; 20-249.  
 DR Ensembl: ENSG00000130076; Homo sapiens.  
 DR InterPro: IPR003599; IG.  
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 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07654; C1-set; 4.  
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 DR SMART: SM00407; IGc1; 3.  
 DR SMART: SM00406; IGv; 1.  
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 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_3.  
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 DB 27 GAGILKPSERTSLTCGVYGSF--SGYWSWIRPPGKGLGEMWIGYHSGNTYVNSLKS 84  
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 DB 85 RVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMQVWGQGLTVVSS 144  
 Search completed: August 30, 2006, 00:35:15  
 Job time : 63.1818 secs

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 15.5455 Seconds  
(without alignments)  
641.891 Million cell updates/sec

Title: US-10-027-725a-9

Sequence: 1 LBSGPGIYKPSQTLSTLCTV.....RSDGYTLDMWGQGLTVVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Database :

Issued Patente\_AA:\*  
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2: /EMC\_Celerra\_SIDS3/prodata/2/1aa/6 COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	2	US-09-049-672A-4
2	515.5	84.0	117	2	US-10-330-613A-13
3	508	82.7	172	2	US-09-472-087-7
4	508	82.7	172	2	US-09-472-087-86
5	507.5	82.7	117	2	US-10-330-613A-5
6	502.5	81.8	119	2	US-09-025-769B-39
7	502.5	81.8	119	2	US-09-025-769B-65
8	502.5	81.8	119	2	US-09-490-070A-39
9	502.5	81.8	119	2	US-09-490-070A-65
10	502.5	81.8	119	2	US-09-490-153-39
11	502.5	81.8	119	2	US-09-490-153-65
12	502.5	81.8	119	2	US-09-490-324-39
13	502.5	81.8	119	2	US-09-490-324-65
14	497.5	81.0	119	2	US-10-330-613A-25
15	496	80.8	122	1	US-08-360-125-11
16	496	80.8	122	1	US-08-450-578-11
17	496	80.8	122	1	US-09-017-628-11
18	496	80.8	122	1	US-09-014-880-11
19	496	80.8	122	2	US-08-450-363-11
20	496	80.8	122	2	US-09-467-903-11
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22	492.5	80.2	117	2	US-09-720-493-2
23	492.5	80.2	117	2	US-10-330-613A-33
24	492	80.1	487	2	US-09-800-729-145
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26	491	80.0	118	2	US-09-490-070A-25

27	491	80.0	118	2	US-09-490-153-25	Sequence 25, Appl
28	491	80.0	118	2	US-09-490-324-25	Sequence 20, Appl
29	491	80.0	120	2	US-09-424-840B-20	Sequence 25, Appl
30	487.5	79.4	119	1	US-08-360-125-5	Sequence 5, Appl
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41	469	76.4	99	2	US-10-194-975-38	Sequence 38, Appl
42	467	76.1	99	2	US-10-194-975-36	Sequence 36, Appl
43	467	76.1	99	2	US-10-194-975-39	Sequence 35, Appl
44	467	76.1	99	2	US-10-330-613A-45	Sequence 45, Appl
45	467	76.1	99	2	US-10-330-613A-57	Sequence 57, Appl

## ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:



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LIBRARY: PANCTUT01
CLONE: 1513264
US-09-049-672a-4

Query Match      84.9%; Score 521; DB 2; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.5e-44;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

Cy 2 ESGGLVPSQTLSTLCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 61
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Cy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSD-----GYTLDMWGCGTLVTVSS 114
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Db 85 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDVGLRGANYGMDVMGCGTLVTVSS 143
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RESULT 2
US-10-330-613A-13
Sequence 13, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: GUDAS, JEAN
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match      84.0%; Score 515.5; DB 2; Length 117;
Best Local Similarity 86.8%; Pred. No. 1.7e-44;
Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;

Cy 2 ESGGLVPSQTLSTLCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGLVPSQTLSTLCTVSGGSIIRSGGYWTWIRHPGKLEWIGIYIYHSGNTYVNSL 65
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Cy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCAR-SCGYTLDMWGCGTLVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSGDGF--DYWGCGTLVTVSS 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-472-087-7
Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT
ORGANISM: Homo Sapiens
```

```
ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      82.7%; Score 508; DB 2; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Cy 3 SGPGLVPSQTLSTLCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 SGPGLVPSQTLSTLCTVSGGSIIRSGGYWSWIRHPGKLEWIGIYIYHSGNTYVNSL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Cy 63 SRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG--YTLDNWGCGTLVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYGIDVWGCGTLVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-09-472-087-86
Sequence 86, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      82.7%; Score 508; DB 2; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Cy 3 SGPGLVPSQTLSTLCTVSGGSIIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVNSL 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 SGPGLVPSQTLSTLCTVSGGSIIRSGGYWSWIRHPGKLEWIGIYIYHSGNTYVNSL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Cy 63 SRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDG--YTLDNWGCGTLVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SRVTISVDTSKNHFSLRLSSVTADTAAYVYCARSDGYGIDVWGCGTLVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-10-330-613A-5
Sequence 5, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: GUDAS, JEAN
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 117
TYPE: PRT
ORGANISM: Homo Sapiens
```



US-10-330-613A-5

Query Match 82.7%; Score 507.5; DB 2; Length 117;

Best Local Similarity 86.8%; Pred. No. 1,1e-43;  
Matches 99; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWMIROPPGKGLMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWMIROPPGKGLMIGIYHSGNTYNNPSL 65  
QY 62 KSRVTISVDTSKNHSIRLSSTVAADTAAYYCAR--SDGYTLDMWGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNHSIRLSSTVAADTAAYYCAR--SDGYTLTVTVSS 117

RESULT 6

US-09-025-769B-39

Sequence 39, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Moroney, Simon

APPLICANT: Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS: linear

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;

Best Local Similarity 85.3%; Pred. No. 3,6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWMIROPPGKGLMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWMIROPPGKGLMIGIYHSGNTYNNPSL 63  
QY 62 KSRVTISVDTSKNHSIRLSSTVAADTAAYYCAR--SDGYTLDMWGQGLTVTVSS 114  
DB 64 KSRVTISVDTSKNHSIRLSSTVAADTAAYYCAR--SDGYTLDMWGQGLTVTVSS 119

RESULT 7

US-09-025-769B-65

Sequence 65, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Moroney, Simon

APPLICANT: Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish &amp; Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;

Best Local Similarity 85.3%; Pred. No. 3,6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWMIROPPGKGLMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYYWMIROPPGKGLMIGIYHSGNTYNNPSL 63  
QY 62 KSRVTISVDTSKNHSIRLSSTVAADTAAYYCAR--SDGYTLDMWGQGLTVTVSS 114  
DB 64 KSRVTISVDTSKNHSIRLSSTVAADTAAYYCAR--SDGYTLDMWGQGLTVTVSS 119

RESULT 8

US-09-490-070A-39

Sequence 39, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Moroney, Simon

APPLICANT: Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-070A-39  
Query Match 81.8%; Score 502.5; DB 2; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3,6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;  
QY 2 ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYNPBL 61  
DB 6 ESGPGLVKPSSETLSTCTVSGSGSIS--YVWSWIRQPPKGLGEMIGYIYSGSTNNPBL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCAR--SDG-YTLDNMGOGTLTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTADTAVYYCARWGSDGFYAMDYWGQTLTVSS 119  
RESULT 9  
US-09-490-070A-65  
Sequence 65, Application US/09490070A  
Patent No. 6696248  
GENERAL INFORMATION:  
ADDRESSEE: Knappik, Achim  
APPLICANT: Knappik, Achim  
Packer, Peter  
Ilag, Vic  
Ge, Liming  
Moreney, Simon  
Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-070A-65  
Query Match 81.8%; Score 502.5; DB 2; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3,6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;  
QY 2 ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWMIROPKGLGEMIGYIYHSGNTYNPBL 61  
DB 6 ESGPGLVKPSSETLSTCTVSGSGSIS--YVWSWIRQPPKGLGEMIGYIYSGSTNNPBL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCAR--SDG-YTLDNMGOGTLTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTADTAVYYCARWGSDGFYAMDYWGQTLTVSS 119  
RESULT 10  
US-09-490-153-39  
Sequence 39, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
ADDRESSEE: Knappik, Achim  
APPLICANT: Knappik, Achim  
Packer, Peter  
Ilag, Vic  
Ge, Liming  
Moreney, Simon  
Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-153-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3.6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYYNPSL 61  
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYYNPSL 63

QY 62 KSRVTMSVDTSKKHFSRLSSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKKHFSRLSSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVSS 119

RESULT 11  
US-09-490-153-65  
Sequence 65, Application US/09490153  
Patent No. 6706484  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthum, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-153-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3.6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYYNPSL 61  
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYYNPSL 63

QY 62 KSRVTMSVDTSKKHFSRLSSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTVSS 114  
Db 64 KSRVTISVDTSKKHFSRLSSVTAADTAVYYCARWGDDGFYAMDYWGQGLTVTVSS 119

RESULT 12  
US-09-490-324-39  
Sequence 39, Application US/09490324  
Patent No. 6828422  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
Ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthum, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-490-324-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;  
Best Local Similarity 85.3%; Pred. No. 3.6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPPGKGLWIGIYHSGNTYYNPSL 61

Db 6 ESGPGLVKSPELTSLTCTVSGSGSISS--YYMSWIRQPPKGLMEIGIYYSGSTNNPSL 63  
Qy 62 KSRVTMSVDTSKNHFSLRLSVTAADTAIVYYCAR--SDG-YTLIDNMGQGLVTYVSS 114  
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYYCARMGDGFYAMDYMGQGLVTYVSS 119

RESULT 13  
US-09-490-324-65  
; Sequence 65, Application US/09490324  
; Patent No. 6828422  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; pack, Peter  
; Ilag, Vlc  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9090  
; TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
US-09-490-324-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;  
Best Local Similarity 85.3%; Pred.No.3.6e-43;  
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy 2 ESGPGLVKSPELTSLTCTVSGSGSISSGGYMSWIRQPPKGLMEIGIYYSGSTNNPSL 61  
Db 6 ESGPGLVKSPELTSLTCTVSGSGSISS--YYMSWIRQPPKGLMEIGIYYSGSTNNPSL 63

Qy 62 KSRVTMSVDTSKNHFSLRLSVTAADTAIVYYCAR--SDG-YTLIDNMGQGLVTYVSS 114  
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAIVYYCARMGDGFYAMDYMGQGLVTYVSS 119

RESULT 14  
US-10-330-613A-25  
; Sequence 25, Application US/10330613A  
; Patent No. 6924360

; GENERAL INFORMATION:  
; APPLICANT: Guddas, Jean  
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN  
; FILE REFERENCE: ABGENTIX.022A  
; CURRENT APPLICATION NUMBER: US/10/330,613A  
; PRIOR FILING DATE: 2002-12-26  
; PRIOR APPLICATION NUMBER: 60/346299  
; PRIOR FILING DATE: 2001-12-18  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 119  
; TYPE: PRP  
; ORGANISM: Homo Sapiens  
US-10-330-613A-25

Query Match 81.0%; Score 497.5; DB 2; Length 119;  
Best Local Similarity 83.3%; Pred.No.1.2e-42;  
Matches 95; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

Qy 2 ESGPGLVKSPELTSLTCTVSGSGSISSGGYMSWIRQPPKGLMEIGIYYSGSTNNPSL 61  
Db 6 ESGPGLVKSPELTSLTCTVSGSGSISSGGYMSWIRQPPKGLMEIGIYYSGSTNNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSVTAADTAIVYYCAR--DGYTLIDNMGQGLVTYVSS 114  
Db 66 KSRVTISVDTSKNQFSLKLSMTAADTAIVYYCARBETAGFPMYMGQGLVTYVSS 119

RESULT 15  
US-08-360-125-11  
; Sequence 11, Application US/08360125  
; Patent No. 5767246  
; GENERAL INFORMATION:  
; APPLICANT: Saiko HOSOKAWA  
; APPLICANT: Yoshiaki TAGAWA  
; APPLICANT: Yoko HIRAKAWA  
; APPLICANT: No. 5767246hiko ITO  
; APPLICANT: Kazuhiko NAGAIKE  
; TITLE OF INVENTION: Human Monoclonal Antibody  
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,125  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/905,534  
; FILING DATE: June 29, 1992  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody 1-3-1  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-360-125-11

Query Match 80.8%; Score 496; DB 1; Length 122;  
Best Local Similarity 81.2%; Pred. No. 1.7e-42;  
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 BSGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPGKLEWIGYIYHSGNTYYNPSL 61  
DB 6 BSGPGLVKPSQTLSTCTVSGSIRSGYYWMIROPGKLEWIGYIYHSGNTYYNPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSD---GYTLDNWGQGLVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARSGYGYGWDWGQGLVTVSS 122

Search completed: August 30, 2006, 00:37:09  
Job time: 16.5455 secs

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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 65.2909 Seconds  
(Without alignments)  
808.788 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LESGPELVKPSQTLSTCTV.....RSDGYTLDMWGQGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*

2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	US-10-027-725A-9	Sequence 9, Appl1
2	600	97.7	114	US-10-027-725A-8	Sequence 8, Appl1
3	556	90.6	114	US-10-027-725A-7	Sequence 7, Appl1
4	524.5	85.4	121	US-10-309-762-152	Sequence 152, App
5	524	85.3	118	US-10-309-762-138	Sequence 138, App
6	523.5	85.3	123	US-10-309-762-10	Sequence 10, Appl
7	521	84.9	120	US-10-309-762-13	Sequence 13, Appl
8	521	84.9	120	US-10-309-762-144	Sequence 144, App
9	521	84.9	122	US-10-309-762-147	Sequence 147, App
10	520	84.6	121	US-09-972-656-80	Sequence 80, Appl
11	519.5	84.6	121	US-10-309-762-151	Sequence 151, App
12	519.5	84.6	125	US-10-309-762-11	Sequence 11, Appl
13	518	84.4	121	US-10-805-177-56	Sequence 56, Appl
14	517.5	84.3	119	US-10-309-762-140	Sequence 140, App
15	517.5	84.3	148	US-11-131-648-13	Sequence 13, Appl
16	517.5	84.3	148	US-11-131-648-35	Sequence 35, Appl
17	517	84.2	125	US-10-805-177-53	Sequence 53, Appl
18	516.5	84.1	123	US-10-309-762-12	Sequence 12, Appl
19	516.5	84.1	144	US-10-893-576-35	Sequence 35, Appl
20	516	84.0	124	US-10-309-762-75	Sequence 75, Appl
21	516	84.0	133	US-10-309-762-96	Sequence 96, Appl
22	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
23	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
24	515.5	84.0	117	US-10-660-357-13	Sequence 13, Appl
25	514	83.7	120	US-10-309-762-128	Sequence 128, App
26	514	83.7	120	US-10-309-762-139	Sequence 139, App
27	514	83.7	121	US-10-308-817-137	Sequence 137, App

28	514	83.7	121	US-10-453-698-137	Sequence 137, App
29	514	83.7	122	US-10-984-960A-56	Sequence 56, Appl
30	513	83.6	116	US-10-309-762-127	Sequence 127, App
31	512.5	83.5	125	US-10-309-762-8	Sequence 8, Appl1
32	512.5	83.5	125	US-10-309-762-16	Sequence 16, Appl
33	512.5	83.5	480	US-10-910-901-6	Sequence 6, Appl1
34	511.5	83.3	119	US-10-309-762-131	Sequence 131, App
35	511.5	83.3	140	US-10-893-576-41	Sequence 41, Appl
36	511	83.2	110	US-10-309-762-74	Sequence 74, Appl
37	510.5	83.1	123	US-10-309-762-9	Sequence 9, Appl1
38	510.5	83.1	127	US-10-309-762-14	Sequence 14, Appl
39	510.5	83.1	148	US-10-893-576-31	Sequence 31, Appl
40	509	82.9	149	US-10-910-901-22	Sequence 22, Appl
41	508.5	82.8	123	US-10-893-576-190	Sequence 190, App
42	508.5	82.8	125	US-10-309-762-153	Sequence 153, App
43	508	82.7	128	US-10-727-155-2	Sequence 2, Appl1
44	508	82.7	128	US-10-727-155-10	Sequence 10, Appl1
45	508	82.7	128	US-10-727-155-30	Sequence 30, Appl1

## ALIGNMENTS

```
RESULT 1
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-9

Query Match      100.0%; Score 614; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LESGPELVKPSQTLSTCTVSGGSIRSGYWSWIRQPGKGLWIGYIYHSNTYVNS 60
      |||
DB      1 LESGPELVKPSQTLSTCTVSGGSIRSGYWSWIRQPGKGLWIGYIYHSNTYVNS 60
      |||

QY      61 LKSRVMSVDTSKNHSFLSSVTADTVYVCARSDGYTLDMWGQGLVTVSS 114
      |||
DB      61 LKSRVMSVDTSKNHSFLSSVTADTVYVCARSDGYTLDMWGQGLVTVSS 114
      |||

RESULT 2
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-027-725A-8

Query Match 97.7%; Score 600; DB 4; Length 114;  
Best Local Similarity 96.5%; Pred. No. 2,4e-46;  
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPS 60  
DB 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114  
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114

RESULT 3  
US-10-027-725A-7

Sequence 7, Application US/10027725A  
Publication No. US20030082659A1

GENERAL INFORMATION:  
APPLICANT: Flicker, Sabine  
TITLE OF INVENTION: Group 2 Allergen Specific IGB-fabs and Use Thereof  
FILE REFERENCE: 25401-4  
CURRENT APPLICATION NUMBER: US/10/027,725A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/259,436  
PRIOR FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-027-725A-7

Query Match 90.6%; Score 556; DB 4; Length 114;  
Best Local Similarity 90.4%; Pred. No. 2,2e-42;  
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPS 60  
DB 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114  
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114

RESULT 4  
US-10-309-762-152

Sequence 152, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 152  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-152

Query Match 85.4%; Score 524.5; DB 4; Length 121;  
Best Local Similarity 86.2%; Pred. No. 1,6e-39;  
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESGPGVLKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPSL 61  
DB 6 ESGPGVLKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114  
DB 66 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 121

RESULT 5  
US-10-309-762-138

Sequence 138, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 138  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-138

Query Match 85.3%; Score 524; DB 4; Length 118;  
Best Local Similarity 88.5%; Pred. No. 1,7e-39;  
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGVLKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPSL 61  
DB 6 ESGPGVLKPSQTLSTLCTVSGGSIRSGGYWMSWIRPPGKGLFEMIGYIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114  
DB 66 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 118

RESULT 6  
US-10-309-762-10

Sequence 10, Application US/10309762  
Publication No. US20040018198A1

GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Foltz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/337275  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-10



Query Match 85.3%; Score 523.5; DB 4; Length 123;  
Best Local Similarity 85.6%; Pred. No. 2e-39;  
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAR---DGYTLDNWGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARAGKTYGSGSYLDYWGQGLTVTVSS 123

## RESULT 7

US-10-309-762-113  
Sequence 113, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Folitz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-113

Query Match 84.9%; Score 521; DB 4; Length 120;  
Best Local Similarity 87.1%; Pred. No. 3.2e-39;  
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAR---LDNMGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCAR-DGYNYWYFDLWGRGTLTVTVSS 120

## RESULT 8

US-10-309-762-144  
Sequence 144, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Folitz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 144  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens

## US-10-309-762-144

Query Match 84.9%; Score 521; DB 4; Length 120;  
Best Local Similarity 87.1%; Pred. No. 3.2e-39;  
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAR---LDNMGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCAR-DGYNYWYFDLWGRGTLTVTVSS 120

## RESULT 9

US-10-309-762-147  
Sequence 147, Application US/10309762  
Publication No. US20040018198A1  
GENERAL INFORMATION:  
APPLICANT: Gudas, Jean  
APPLICANT: Folitz, Ian  
APPLICANT: Handa, Masahisa  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
FILE REFERENCE: ABGENIX.027A  
CURRENT APPLICATION NUMBER: US/10/309,762  
CURRENT FILING DATE: 2002-12-02  
PRIOR FILING DATE: 2001-12-03  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 147  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-309-762-147

Query Match 84.9%; Score 521; DB 4; Length 122;  
Best Local Similarity 85.5%; Pred. No. 3.3e-39;  
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGYWSWIRPPGKGLWIGIYHSGNTYNNPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCAR---SDGYTLDNWGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARYYDILTYGMDVWGQGLTVTVSS 122

## RESULT 10

US-09-972-656-80  
Sequence 80, Application US/09972656  
Publication No. US20030099647A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Tsai, Wei-Wei  
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
FILE REFERENCE: A-799  
CURRENT APPLICATION NUMBER: US/09/972,656  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 80  
LENGTH: 221  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-972-656-80

Query Match 84.7%; Score 520; DB 3; Length 221;

Best Local Similarity 86.7%; Pred. No. 7.3e-39;  
 Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
 Db 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61  
 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114  
 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 118  
 Db

RESULT 11  
 US-10-309-762-151  
 ; Sequence 151, Application US/10309762  
 ; Publication No. US20040018196A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; APPLICANT: Foltz, Ian  
 ; APPLICANT: Handa, Masahisa  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
 ; FILE REFERENCE: ABGENIX.027A  
 ; CURRENT APPLICATION NUMBER: US/10/309,762  
 ; CURRENT FILING DATE: 2002-12-02  
 ; PRIOR APPLICATION NUMBER: 60/337275  
 ; PRIOR FILING DATE: 2001-12-03  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 151  
 ; LENGTH: 121  
 ; TYPE: PRP  
 ; ORGANISM: Homo sapiens  
 US-10-309-762-151

Query Match 84.6%; Score 519.5; DB 4; Length 121;  
 Best Local Similarity 86.2%; Pred. No. 4.4e-39;  
 Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;  
 Db 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61  
 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114  
 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 121  
 Db

RESULT 12  
 US-10-309-762-11  
 ; Sequence 11, Application US/10309762  
 ; Publication No. US20040018196A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; APPLICANT: Foltz, Ian  
 ; APPLICANT: Handa, Masahisa  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
 ; FILE REFERENCE: ABGENIX.027A  
 ; CURRENT APPLICATION NUMBER: US/10/309,762  
 ; CURRENT FILING DATE: 2002-12-02  
 ; PRIOR APPLICATION NUMBER: 60/337275  
 ; PRIOR FILING DATE: 2001-12-03  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 125  
 ; TYPE: PRP  
 ; ORGANISM: Homo sapiens  
 US-10-309-762-11

Query Match 84.6%; Score 519.5; DB 4; Length 125;  
 Best Local Similarity 83.3%; Pred. No. 4.6e-39;  
 Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;  
 Db 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61  
 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114  
 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 125  
 Db

RESULT 13  
 US-10-805-177-56  
 ; Sequence 56, Application US/10805177  
 ; Publication No. US2005008449A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Landes, Gregory M.  
 ; APPLICANT: Chen, Francine  
 ; APPLICANT: Bezabeh, Binham  
 ; APPLICANT: Foltz, Ian  
 ; APPLICANT: Tse, Kam Fai  
 ; APPLICANT: Jeffers, Michael  
 ; APPLICANT: Meiri, Mehdi  
 ; APPLICANT: Starling, Gary  
 ; APPLICANT: Mezes, Peter  
 ; APPLICANT: Khramtsov, Nikolai  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN  
 ; FILE REFERENCE: ABXCUR.006A  
 ; CURRENT APPLICATION NUMBER: US/10/805,177  
 ; CURRENT FILING DATE: 2004-03-19  
 ; PRIOR APPLICATION NUMBER: 60/456,652  
 ; PRIOR FILING DATE: 2003-03-19  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 56  
 ; LENGTH: 121  
 ; TYPE: PRP  
 ; ORGANISM: Homo Sapiens  
 US-10-805-177-56

Query Match 84.4%; Score 518; DB 5; Length 121;  
 Best Local Similarity 84.3%; Pred. No. 6.1e-39;  
 Matches 97; Conservative 9; Mismatches 7; Indels 2; Gaps 1;  
 Db 2 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 61  
 6 ESEPGLVKPSQTLSTCTVSGGSIIRSGGYWSWIRPPGKGLWIGIYHSGNTYNPSTL 65  
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 114  
 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAAYVYCARSDGY--TLDMNGOGTLVTVSS 120  
 Db

RESULT 14  
 US-10-309-762-140  
 ; Sequence 140, Application US/10309762  
 ; Publication No. US20040018196A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gudas, Jean  
 ; APPLICANT: Foltz, Ian  
 ; APPLICANT: Handa, Masahisa  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX  
 ; FILE REFERENCE: ABGENIX.027A  
 ; CURRENT APPLICATION NUMBER: US/10/309,762  
 ; CURRENT FILING DATE: 2002-12-02  
 ; PRIOR APPLICATION NUMBER: 60/337275  
 ; PRIOR FILING DATE: 2001-12-03  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 140  
 ; LENGTH: 125  
 ; TYPE: PRP  
 ; ORGANISM: Homo sapiens  
 US-10-309-762-140

SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-309-762-140

Query Match 84.3%; Score 517.5; DB 4; Length 119;  
Best Local Similarity 86.8%; Pred. No. 6,6e-39;  
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 61  
DB 6 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 65  
QY 62 KSRVTWSVDTSKNHFSLRLSSVTAAADTAVYYCARSD-GYTLDNWGQGLTVTVSS 114  
DB 66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARGNYYGMDVWGQGLTVTVSS 119

## RESULT 15

US-11-131-648-13  
; Sequence 13, Application US/11131648  
; Publication No. US20050221400A1  
; GENERAL INFORMATION:  
; APPLICANT: Gudas, Jean  
; APPLICANT: Jakobovits, Aya  
; APPLICANT: Xiao-Chi, Jia  
; APPLICANT: Morrison, Robert Kendall  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Shao, Hui  
; APPLICANT: Chailita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO BSCA PROTEINS  
; FILE REFERENCE: 51158-20088.20  
; CURRENT APPLICATION NUMBER: US/11/131,648  
; PRIOR FILING DATE: 2005-05-17  
; PRIOR APPLICATION NUMBER: 60/616,381  
; PRIOR FILING DATE: 2004-10-05  
; PRIOR APPLICATION NUMBER: 60/617,881  
; PRIOR FILING DATE: 2004-10-12  
; PRIOR APPLICATION NUMBER: 60/621,310  
; PRIOR FILING DATE: 2004-10-21  
; PRIOR APPLICATION NUMBER: 60/633,077  
; PRIOR FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: 10/857,484  
; PRIOR FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: 60/475,064  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-131-648-13

Query Match 84.3%; Score 517.5; DB 6; Length 148;  
Best Local Similarity 83.5%; Pred. No. 8.2e-39;  
Matches 101; Conservative 4; Mismatches 7; Indels 9; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 61  
DB 15 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYVPSL 74  
QY 62 KSRVTWSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-----YTLDNWGQGLTVTVSS 113  
DB 75 KSRVTWSVDTSKNQFSLKLSSTVTAADTAVYYCAR-DEITMIRGYYGMDVWGQGLTVTVSS 133  
QY 114 S 114  
DB 134 S 134

Search completed: August 30, 2006, 00:50:38  
Job time : 66.2909 secs

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GenCore version 5.1.9.  
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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 13.4727 Seconds

(without alignments)  
578.960 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LBSGPGLVKPSQTLSTLCTV.....RSDGYTLDMWGQGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_NEW\_PUB.dep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US06\_NEW\_PUB.dep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_NEW\_PUB.dep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_NEW\_PUB.dep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/PCT\_NEW\_PUB.dep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_NEW\_PUB.dep:\*
- 7: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_NEW\_PUB.dep:\*
- 8: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US60\_NEW\_PUB.dep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	85.4	118	6	US-10-981-300-51 Sequence 51, App1
2	502.5	81.8	119	7	US-11-304-986-25 Sequence 25, App1
3	501.5	81.7	149	7	US-11-355-464-13 Sequence 13, App1
4	501.5	81.7	149	7	US-11-355-464-16 Sequence 16, App1
5	497.5	81.0	121	7	US-11-337-300-84 Sequence 84, App1
6	497.5	81.0	248	7	US-11-337-300-94 Sequence 94, App1
7	495.5	80.7	121	7	US-11-211-917-82 Sequence 82, App1
8	495.5	80.7	466	7	US-11-211-917-86 Sequence 86, App1
9	493.5	80.4	121	7	US-11-211-917-98 Sequence 98, App1
10	493.5	80.4	466	7	US-11-211-917-70 Sequence 70, App1
11	492	80.1	118	7	US-11-211-917-109 Sequence 109, App1
12	492	80.1	118	7	US-11-211-917-109 Sequence 109, App1
13	492	80.1	120	7	US-11-211-917-142 Sequence 142, App1
14	491.5	80.0	121	7	US-11-211-917-66 Sequence 66, App1
15	490.5	79.9	118	6	US-10-981-300-52 Sequence 52, App1
16	490.5	79.9	180	6	US-10-981-300-4 Sequence 4, App1
17	489	79.6	115	6	US-10-981-300-53 Sequence 53, App1
18	489	79.6	126	6	US-10-994-679-68 Sequence 68, App1
19	485.5	79.1	121	7	US-11-211-917-26 Sequence 26, App1
20	485.5	79.1	466	7	US-11-211-917-30 Sequence 30, App1
21	483	78.7	108	7	US-11-281-266-82 Sequence 82, App1
22	479.5	78.1	107	6	US-10-484-105-18 Sequence 18, App1
23	476.5	77.6	118	6	US-10-981-300-54 Sequence 54, App1
24	476.5	77.6	443	6	US-10-981-300-20 Sequence 20, App1
25	476	77.5	120	7	US-11-211-917-108 Sequence 108, App1

26	474.5	77.3	113	7	US-11-290-687-17 Sequence 17, App1
27	474	77.2	247	6	US-10-539-402-10 Sequence 10, App1
28	473.5	77.1	119	7	US-11-211-917-18 Sequence 18, App1
29	473.5	77.1	464	7	US-11-211-917-22 Sequence 22, App1
30	472	76.9	244	7	US-11-402-010-77 Sequence 77, App1
31	471.5	76.8	121	6	US-10-994-679-60 Sequence 60, App1
32	468	76.2	108	7	US-11-281-266-85 Sequence 85, App1
33	467	76.1	286	7	US-11-154-103-8 Sequence 8, App1
34	465	75.7	444	7	US-11-317-786B-17 Sequence 17, App1
35	465	75.7	248	7	US-11-317-786B-9 Sequence 9, App1
36	461.5	75.2	197	1	US-09-784-950-25 Sequence 25, App1
37	459.5	74.8	117	7	US-11-290-687-41 Sequence 41, App1
38	459.5	74.8	127	7	US-11-259-133-202 Sequence 202, App1
39	458	74.6	124	7	US-11-111-688-1 Sequence 1, App1
40	458	74.6	126	7	US-11-111-688-55 Sequence 55, App1
41	458	74.6	244	7	US-11-317-786B-19 Sequence 19, App1
42	458	74.6	448	7	US-11-317-786B-11 Sequence 11, App1
43	457	74.4	240	7	US-11-317-786B-15 Sequence 15, App1
44	457	74.4	445	7	US-11-317-786B-32 Sequence 32, App1
45	457	74.4	448	7	US-11-317-786B-7 Sequence 7, App1

## ALIGNMENTS

```
RESULT 1
US-10-981-300-51
; Sequence 51, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-300-51

Query Match      85.4%; Score 524.5; DB 6; Length 118;
Best Local Similarity 88.5%; Pred. No. 1.4e-39;
Matches 100; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY      2  ESQPGLVKPSQTLSTLCTVSGSIRSGYYWMIROPGKLEWIGYVHSGNTYNNPSL 61
DB      6  ESQPGLVKPSQTLSTLCTVSGSIRSGYYWMIROPGKLEWIGYVHSGNTYNNPSL 65

QY      62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
DB      66 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 117

RESULT 2
US-11-304-986-25
; Sequence 25, Application US/11304986
; Publication No. US20060165682A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth and Neirajab et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; FILE REFERENCE: ELN-055
; CURRENT APPLICATION NUMBER: US/11/304,986
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: 60/636684
; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct, consensus sequence for heavy chain
; OTHER INFORMATION: framework region
US-11-304-986-25
```

```
Query Match      81.8%; Score 502.5; DB 7; Length 119;
Best Local Similarity 85.3%; Pred. No. 1.3e-37;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;
```

```
QY 2 ESGGLVPSQTLSTCTVSGGSIIRSGYWSWIRPPGKGLWIGIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGGLVPSQTLSTCTVSGGSIIS--YWSWIRPPGKGLWIGIYHSGNTYVNSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCAR--SDG-YTLDNMGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 KSRVTISVDTSKNQPFLKLSSTVTAADTAVYYCARMGDGFYANDYWGQGLTVTVSS 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 3
US-11-355-464-13
; Sequence 13, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: CHALILITA-EID, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT FILING DATE: 2006-02-15
; PRIOR FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US 11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-355-464-13
```

```
Query Match      81.7%; Score 501.5; DB 7; Length 149;
Best Local Similarity 81.8%; Pred. No. 1.9e-37;
Matches 99; Conservative 5; Mismatches 8; Indels 9; Gaps 2;
```

```
QY 2 ESGGLVPSQTLSTCTVSGGSIIRSGYWSWIRPPGKGLWIGIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 ESGGLVPSQTLSTCTVSGGSIISGGYWSWIRQHFGKGLWIGIYHSGNTYVNSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYT-----LDNMGQGLTVTVS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 KSRVTISVDTSKNQPFLKLSSTVTAADTAVYYCAR-DHITWRGVKGMVDYWGQGLTVTVS 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 114 S 114
Db 123 S 123
```

```
RESULT 4
US-11-355-464-16
; Sequence 16, Application US/11355464
; Publication No. US20060147375A1
; GENERAL INFORMATION:
; APPLICANT: GUDAS, Jean
; APPLICANT: JAKOBOVITS, Aya
; APPLICANT: JIA, Xiao-Chi,
; APPLICANT: MORRISON, Robert Kendall
; APPLICANT: CHALILITA-EID, Pia M.
; APPLICANT: RAITANO, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT
; FILE REFERENCE: 511582008821
; CURRENT APPLICATION NUMBER: US/11/355,464
; CURRENT FILING DATE: 2006-02-15
; PRIOR APPLICATION NUMBER: US 11/131,648
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/672,000
; PRIOR FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: US 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-355-464-16
```

```
Query Match      81.7%; Score 501.5; DB 7; Length 149;
Best Local Similarity 81.8%; Pred. No. 1.9e-37;
Matches 99; Conservative 5; Mismatches 8; Indels 9; Gaps 2;
```

```
QY 2 ESGGLVPSQTLSTCTVSGGSIIRSGYWSWIRPPGKGLWIGIYHSGNTYVNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 ESGGLVPSQTLSTCTVSGGSIISGGYWSWIRQHFGKGLWIGIYHSGNTYVNSL 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYT-----LDNMGQGLTVTVS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 KSRVTISVDTSKNQPFLKLSSTVTAADTAVYYCAR-DHITWRGVKGMVDYWGQGLTVTVS 122
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 114 S 114
Db 123 S 123
```

```
RESULT 5
US-11-337-300-84
; Sequence 84, Application US/11337300
; Publication No. US20060121580A1
; GENERAL INFORMATION:
; APPLICANT: Cruceil Holland B.V.
; APPLICANT: ter Meulen, Jan H.
; APPLICANT: De Kruijf, Cornelis A.
; APPLICANT: van den Brink, Edward N.
; APPLICANT: Goudsmilt, Jaap
```

;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
;; FILE REFERENCE: 0091 WO 00 ORD  
;; CURRENT APPLICATION NUMBER: US/11/337,300  
;; CURRENT FILING DATE: 2006-01-20  
;; NUMBER OF SEQ ID NOS: 478  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 84  
;; LENGTH: 121  
;; TYPE: PRN  
;; ORGANISM: Artificial sequence  
;; OTHER INFORMATION: Variable heavy chain of SC03-017  
US-11-337-300-84

Query Match 81.0%; Score 497.5; DB 7; Length 121;  
Best Local Similarity 83.5%; Pred. No. 3.5e-37;  
Matches 96; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61  
DB 8 ESGAGLKPSETISLTCTVSGSVSGSYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 67  
QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCA--RSDGYTLDNWGGTLVTYSS 114  
DB 68 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCAKRSRAGF-FDYWGCGTLVTYSS 121

RESULT 6  
US-11-337-300-94  
;; Sequence 94; Application US/11337300  
;; Publication No. US20060121580A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Crucell Holland B.V.  
;; APPLICANT: ter Meulen, Jan H.  
;; APPLICANT: De Kruif, Cornelis A.  
;; APPLICANT: van den Brink, Edward N.  
;; APPLICANT: Goudemil, Jaap  
;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
;; FILE REFERENCE: 0091 WO 00 ORD  
;; CURRENT APPLICATION NUMBER: US/11/337,300  
;; CURRENT FILING DATE: 2006-01-20  
;; NUMBER OF SEQ ID NOS: 478  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 94  
;; LENGTH: 248  
;; TYPE: PRN  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: SC03-017  
US-11-337-300-94

Query Match 81.0%; Score 497.5; DB 7; Length 248;  
Best Local Similarity 83.5%; Pred. No. 7e-37;  
Matches 96; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61  
DB 9 ESGAGLKPSETISLTCTVSGSVSGSYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 68  
QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCA--RSDGYTLDNWGGTLVTYSS 114  
DB 69 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCAKRSRAGF-FDYWGCGTLVTYSS 122

RESULT 7  
US-11-211-917-82  
;; Sequence 82; Application US/11211917  
;; Publication No. US20060093600A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BEDIAN, VAHE  
;; APPLICANT: GLADUE, RONALD P.  
;; APPLICANT: CORVALAN, JOSE  
;; APPLICANT: JIA, XIAO-CHI

;; APPLICANT: FENG, XIAO  
;; TITLE OF INVENTION: ANTIBODIES TO CD40  
;; FILE REFERENCE: ABX-PP/3 US  
;; CURRENT APPLICATION NUMBER: US/11/211,917  
;; CURRENT FILING DATE: 2005-08-25  
;; PRIOR APPLICATION NUMBER: US/10/292,088  
;; PRIOR FILING DATE: 2002-11-08  
;; PRIOR APPLICATION NUMBER: 60/348,980  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 82  
;; LENGTH: 121  
;; TYPE: PRN  
;; ORGANISM: Homo sapiens  
US-11-211-917-82

Query Match 80.7%; Score 495.5; DB 7; Length 121;  
Best Local Similarity 83.1%; Pred. No. 5.3e-37;  
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61  
DB 6 ESGPGLVPSQTLSTCTVSGSIR--GYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 63  
QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCARSDGYTLD-----NWGGTLVTYSS 114  
DB 64 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCARRGGLYGDYGFAPWGGTLVTYSS 121

RESULT 8  
US-11-211-917-86  
;; Sequence 86; Application US/11211917  
;; Publication No. US20060093600A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BEDIAN, VAHE  
;; APPLICANT: GLADUE, RONALD P.  
;; APPLICANT: CORVALAN, JOSE  
;; APPLICANT: JIA, XIAO-CHI  
;; APPLICANT: FENG, XIAO  
;; TITLE OF INVENTION: ANTIBODIES TO CD40  
;; FILE REFERENCE: ABX-PP/3 US  
;; CURRENT APPLICATION NUMBER: US/11/211,917  
;; CURRENT FILING DATE: 2005-08-25  
;; PRIOR APPLICATION NUMBER: US/10/292,088  
;; PRIOR FILING DATE: 2002-11-08  
;; PRIOR APPLICATION NUMBER: 60/348,980  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 147  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 86  
;; LENGTH: 466  
;; TYPE: PRN  
;; ORGANISM: Homo sapiens  
US-11-211-917-86

Query Match 80.7%; Score 495.5; DB 7; Length 466;  
Best Local Similarity 83.1%; Pred. No. 1.9e-36;  
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61  
DB 25 ESGPGLVPSQTLSTCTVSGSIR--GYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 82  
QY 62 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCARSDGYTLD-----NWGGTLVTYSS 114  
DB 83 KSRVTSVDTSKNHFSLRLSSVTADTAAYYCARRGGLYGDYGFAPWGGTLVTYSS 140

RESULT 9  
US-11-211-917-98  
;; Sequence 98; Application US/11211917  
;; Publication No. US20060093600A1

Query Match	80.4%	Score	493.5	DB 7	Length	121
Best Local Similarity	82.2%	Pred. No.	7.9e-37			
Matches	97	Conservative	6	Mismatches	8	Indels
						Gaps
						2
QY	2	ESGPELVMPSPQSLITCTVYSSGSGIRSGGYWMIROPGKGLWEVIGYIHSGNTYNSL	61			
DB	6	ESGPELVMPSESLITCTVYSSGSGIR--GYWMIROPGKGLWEVIGYIHSGNTYNSL	63			
QY	62	KSRVTASVDTSGNHSLSKLSVTAADTVAYVYCARBDGYLD---- <td>114</td> <td></td> <td></td> <td></td>	114			
DB	64	KSRVITSVDTSGNQSLKLSVTAADTVAYVYCARKGGLYGDYGMFAPMCGGLTVSS	121			

QY 2 EGGPGVAKSQTLSLCTVSGGSGIRGGYMSWIRPPGKGLMIIDYIIHSHANTYINPSL 61

Db 25 EGGPGVAKSESLTCTCTVSGGSR--GYMSWIRPPGKGLMIIDYIIYSGSTINPSL 82

QY 62 KRRYMSYPTSKHSESLSSVTAADTAYVYCARSRGTYLD-----NMGGTLTYVSS 114

Db 83 KRRVITSVPTSKQFSLKNSVTAADTAYVYCARRGSLYEDYGMFAPMGGTLTYVSS 140

	Query Match	Similarity	80.1%	Score 492;	DB 7;	Length 118;
	Best Local	Similarity	84.3%	Pred. No. 1,1e-36;		
	Matches	Conservative	5;	Indels	4;	Gaps 2;
CY	2	ESGPGVWPSTLTLCTCGSGSIRSGGYMSWIROPKGKLEWIGIYHSGNTYNSPL	61			
DB	6	ESGGLVPSPSTLSLTCTVCSGGIS--YYMSWIROPKGKLEWIGIYHSGNINPSL	63			
CY	62	KSRVTMSVDTSKNHPSLRSLSVTAADPAVVYCARSDGYT--LDNWGGSTLVTVSS	114			
DB	64	KSRVTISVDTSKNQPSLRSLSVTAADIAVVYCAARDYGNSITFDWGGSTLVTVSS	118			

	Query Match	Similarity	Score	DB	Length
Best Local	80.1%	85.2%	492	7	118
Matches	98	Conservative	5	Mismatches	8
				Indels	4
				Gaps	3



QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLTVTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARDYGDYWFPGKGLTVTVSS 118

## RESULT 13

US-11-281-266-6  
Sequence 6, Application US/11281266  
Publication No. US20060140948A1

GENERAL INFORMATION:  
APPLICANT: Foltz, Ian  
APPLICANT: Fagioni, Raffaella  
APPLICANT: Senaldi, Giorgio  
APPLICANT: Manchulenko, Kathy  
APPLICANT: Kang, Jaspal  
APPLICANT: Rathnaswami, Palaniswami  
APPLICANT: Anilwalia, Kiran  
APPLICANT: Food, Oric  
APPLICANT: Klakamp, Scott  
TITLE OF INVENTION: FULLY HUMAN MONOCLONAL ANTIBODIES TO  
TITLE OF INVENTION: IL-13  
FILE REFERENCE: ABGENIX.119A  
CURRENT APPLICATION NUMBER: US/11/281,266  
CURRENT FILING DATE: 2005-11-16  
PRIOR APPLICATION NUMBER: 60/629,135  
PRIOR FILING DATE: 2004-11-17  
PRIOR APPLICATION NUMBER: 60/728,604  
PRIOR FILING DATE: 2005-10-19  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-281-266-6

Query Match 80.1%; Score 492; DB 7; Length 120;  
Best Local Similarity 81.2%; Pred. No. 1,1e-36;

Matches 95; Conservative 8; Mismatches 8; Indels 6; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWMIROPKGLGEMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGSIST--YYWMIROPKGLGEMIGIYHSGNTYNNPSL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLTVTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARDYGDYWFPGKGLTVTVSS 120

## RESULT 14

US-11-211-917-66  
Sequence 66, Application US/11211917  
Publication No. US20060093600A1

GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JTA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/11/211,917  
CURRENT FILING DATE: 2005-08-25  
PRIOR APPLICATION NUMBER: US/10/292,088  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 66  
LENGTH: 121  
TYPE: PRT

ORGANISM: Homo sapiens  
US-11-211-917-66

Query Match 80.0%; Score 491.5; DB 7; Length 121;  
Best Local Similarity 82.2%; Pred. No. 1.2e-36;  
Matches 97; Conservative 5; Mismatches 9; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWMIROPKGLGEMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGSIR--GYWMIROPKGLGEMIGIYHSGNTYNNPSL 63  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLTVTVSS 114  
DB 64 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARDYGDYWFPGKGLTVTVSS 121

## RESULT 15

US-10-981-300-52  
Sequence 52, Application US/10981300  
Publication No. US20060093599A1

GENERAL INFORMATION:  
APPLICANT: GIORGIO SENALDI  
APPLICANT: GADI GAZIT-BORSTEIN  
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
FILE REFERENCE: ABGX-005  
CURRENT APPLICATION NUMBER: US/10/981,300  
CURRENT FILING DATE: 2004-11-03  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52  
LENGTH: 118  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-981-300-52

Query Match 79.9%; Score 490.5; DB 6; Length 118;  
Best Local Similarity 82.3%; Pred. No. 1.4e-36;  
Matches 93; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGSIRSGYYWMIROPKGLGEMIGIYHSGNTYNNPSL 61  
DB 6 ESGPGLVKPSQTLSTLCTVSGDISISGYYWMIROHPKGLGEMIGIYHSGNTYNNPSL 65  
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSDG-YT-LDNGGGLTVTVSS 114  
DB 66 KSRFTISVDTSKNQFSLKLSVTAAADTAVYYCARDYD-FDIWGLGGLTVTVSS 117

Search completed: August 30, 2006, 00:52:02  
Job time: 14.4727 secs

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PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IGG comprising  
PT variable region of group 2 allergen specific-human IGE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.

XX Disclosure; Page 39; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IGE Fabs and methods for their use. The proteins  
CC of the invention may have antiallergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IGE  
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IGE antibodies to Phi p 2. The present sequence represents the human IGE  
CC Fab, clone 94 light chain protein of the invention

XX Sequence 106 AA;

SQ Query Match 98.2%; Score 533; DB 5; Length 106;

Best Local Similarity 99.1%; Pred. No. 5.6e-33; Mismatches 1; Indels 0; Gaps 0;

Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVNTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60

Db 1 ELTQSPSSLSASVGDVNTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60

QY 61 SSGSGYGFDTFTLTISLQFEDFASVYCOESLSASTFGQGTVEIKR 106

Db 61 SSGSGYGFDTFTLTISLQFEDFASVYCOESLSASTFGQGTVEIKR 106

RESULT 2  
AAR54260  
ID AAR54260 standard; protein; 107 AA.

XX AAR54260;

XX AC 25-MAR-2003 (revised)

DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b22.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KW neutralisation; monoclonal antibody; kappa light chain; variable region;

KW framework; complementarity determining region.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..21 /label= FR1

FT 22..33 /label= CDR1

FT 34..48 /label= FR2

FT 49..55 /label= FR2

FT 56..87 /label= CDR2

FT 88..95 /label= FR3

FT 96..107 /label= CDR3

FT 96..107 /label= FR4

XX Region

XX Region

PD 14-APR-1994.

XX 30-SEP-1993; 93WO-US009328.

XX 30-SEP-1992; 92US-00954148.

XX (SCRI ) SCRIPPS RES INST.

PI Burton DR, Barbas CF, Lerner RA;

XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or

PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro

PT diagnosis and for passive immuno-therapy.

XX Claim 5; Page 189; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification

CC using primers specific for heavy and light chain variable regions. The

CC amplification products were inserted into a distronic vector to produce

CC a library of fragments. E.coli XL1 Blue cells were transformed with the

CC library. Filamentous phage were produced which expressed the MAb regions

CC on their surface. Panning with gp120 and gp41 resulted in the recovery of

CC immunoreactive clones. The light chain VK region sequence AAR54260

CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 107 AA;

SQ Query Match 87.5%; Score 475; DB 2; Length 107;

Best Local Similarity 87.7%; Pred. No. 1.4e-28; Mismatches 7; Indels 0; Gaps 0;

Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVNTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60

Db 1 ELTQSPSSLSASVGDVNTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60

QY 61 SSGSGYGFDTFTLTISLQFEDFASVYCOESLSASTFGQGTVEIKR 106

Db 61 SSGSGYGFDTFTLTISLQFEDFASVYCOESLSASTFGQGTVEIKR 106

RESULT 3  
AAM01283  
ID AAM01283 standard; protein; 107 AA.

XX AAM01283;

XX AC 29-JAN-1997 (first entry)

DT VL region of HIV neutralising MAb, clone b22 and B35.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;

KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KW virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..21 /label= FR1

FT 22..32 /label= CDR1

FT 33..47 /label= FR2

FT 48..54 /label= FR2

FT 55..86 /label= CDR2

FT 87..95 /label= FR3

FT 96..107 /label= CDR3

FT 96..107 /label= FR4

XX Region

XX Region

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FT XX /label= FR4
XX XX
XX PN MO9602273-A1.
XX XX
XX PD 01-FEB-1996.
XX XX
XX PF 11-JUL-1995; 95WO-US008743.
XX XX
XX PR 18-JUL-1994; 94US-00276852.
XX XX
XX PA (SCRI ) SCRIPPS RES INST.
XX XX
XX PI Burton DR, Barbas CF, Lerner RA;
XX XX
XX DR MPI, 1996-179601/18.
XX XX
XX PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
XX XX immunotherapy and detection of HIV infection.
XX XX
XX PS Example; Fig 11; 366pp; English.
XX XX
CC The sequences given in AA01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JH2 gene
CC clones, b22 and B35. A Mab containing this VL sequence has the capacity
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by
CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds
CC mature gp120 preferentially over the precursor gp160. The Mab may be used
CC for determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
CC XX
SQ Sequence 107 AA;

Query Match 87.5%; Score 475; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASORINTYLMVYQHKPGKAPKLLIYAASSLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITCRASQSISSYLMVYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SSGSGYGTDFTLTITSSLQPEDFASVYCOESLSASVYTFGCGTKVEIKR 106
DB 61 SSGSGGTDFTLTITSSLQPEDFATVYCOQSYSTPYTFGCGTKLEIKR 106

RESULT 4
AA98244
ID AA98244 standard; protein; 107 AA.
AC AA98244;
XX
XX 04-JUL-2000 (first entry)
XX
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX
XX KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX passive immunotherapy; reduce severity; HIV-induced disease;
XX immunocompetence; active immunisation.
XX
XX OS Homo sapiens.
XX
XX AC AU9948754-A.
XX
XX PD 17-FEB-2000.
XX
XX PF 16-SEP-1999; 99AU-00048754.
XX
XX PR 16-SEP-1999; 99AU-00048754.
XX
XX PA (SCRI ) SCRIPPS RES INST.

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XX XX
XX PI Burton DR, Barbas CF, Lerner RA;
XX XX
XX DR MPI, 2000-246867/22.
XX XX
XX PT Human neutralising monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX
XX PS Example 9; Fig 11; 374pp; English.
XX
CC This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
CC of reducing an HIV infectivity titre in an in vitro virus infectivity
CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
CC production of the antibody comprises: (a) providing a first
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
CC (which does not comprise the sequence represented by AA98206) and a
CC second polynucleotide encoding a light chain immunoglobulin amino acid
CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provide information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
CC XX
SQ Sequence 107 AA;

Query Match 87.5%; Score 475; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASORINTYLMVYQHKPGKAPKLLIYAASSLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITCRASQSISSYLMVYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SSGSGYGTDFTLTITSSLQPEDFASVYCOESLSASVYTFGCGTKVEIKR 106
DB 61 SSGSGGTDFTLTITSSLQPEDFATVYCOQSYSTPYTFGCGTKLEIKR 106

RESULT 5
AA95135
ID AA95135 standard; protein; 107 AA.
AC AA95135;
XX
XX 30-JUN-2000 (first entry)
XX
XX DE Anti-gp120 antibody light chain variable region from clone b22.
XX
XX KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
XX OS Homo sapiens.

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XX
PN AU9948756-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-00048756.
XX
PR 16-SEP-1999; 99AU-00048756.
XX
PA (SCRI ) SCRIAPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-293393/26.
XX
PT Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
XX
PS Example 9; Fig 11; 366bp; English.
XX
CC The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
XX
SQ Sequence 107 AA;
Query Match 87.5%; Score 475; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNMYQHKRGKAPKLLIYAASLSGVP5RF 60
DB 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNMYQHKRGKAPKLLIYAASLSGVP5RF 60
QY 61 SGGSGYGDPTLTSSLOFEPASYYCOESLSASTYFQGTVEIKR 106
DB 61 SGGSGYGDPTLTSSLOFEPASYYCOESLSASTYFQGTVEIKR 106
RESULT 6
AEF65392
ID AEF65392 standard; protein; 214 AA.
XX
AC AEF65392;
XX
DT 06-APR-2006 (first entry)
XX
DE Anti-Rhd Fab clone Rhd200.164G10 Lc region sequence.
XX
KW antibody engineering; anti-Rhesus D antibody; anti-Rhd antibody;

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```

KW Gene expression; hemostatic; therapeutic; newborn hemolytic disease;
KW thrombocytopenic purpura; TRP; antibody.
XX
OS Homo sapiens.
XX
PN WO2006007850-A1.
XX
PD 26-JAN-2006.
XX
PF 18-JUL-2005; 2005WO-DK000501.
XX
PR 20-JUL-2004; 2004DK-00001133.
XX
PR 22-DEC-2004; 2004DK-00001992.
XX
PA (SYMP-) SYMPHOGEN AS.
XX
PI Rasmussen SK, Tolstrup AB, Frederiksen SB, Haurum U;
XX
DR WPI; 2006-110334/11.
XX
DR N-PSDB; AEF65280.
XX
PT Generating a collection of cells for expression of anti-Rhesus D
PT recombinant polyclonal antibodies, involves selecting cells having
PT integrated copy of antibody-encoding nucleic acid from library of anti-
PT Rhd antibody expression vectors.
XX
PS Example 1; SEQ ID NO 221; 245bp; English.
XX
CC The invention relates to generating (M1) a collection of cells suitable
CC as manufacturing cell line for expression of anti-Rhesus D (Rhd)
CC recombinant polyclonal antibody. The method involves introducing a
CC library of anti-Rhd antibody expression vectors into a host cell line,
CC and selecting cells comprising an integrated copy of the anti-Rhd
CC antibody-encoding nucleic acid segment from the library of anti-Rhd
CC antibody expression vectors, where each individual vector of library
CC comprises one single copy of a nucleic acid segment encoding a distinct
CC member of the anti-Rhd polyclonal antibody, and one or more recombinase
CC recognition sequences. Methods are also provided for generating (M2) a
CC polyclonal working cell bank; manufacturing (M3) an anti-Rhd recombinant
CC polyclonal antibody. In (M1), the library of anti-Rhd antibody expression
CC vectors encodes an anti-Rhd recombinant polyclonal antibody where at
CC least one of the individual members specifically bind to ePD3, ePD4, and
CC ePD9 (Rhd category VI antigen) and further members alone or in
CC combination bind to the remaining Rhesus D antigen epitopes ePD1, ePD2,
CC ePD5, ePD6/7 and ePD8. The single copy of a nucleic acid segment encoding
CC a distinct member of the anti-Rhd polyclonal, is integrated in a single
CC predefined genomic locus of each individual cell in the collection of
CC cells, the locus being capable of mediating high-level expression of each
CC member of the recombinant polyclonal antibody. (M1) is useful for
CC generating a collection of cells suitable as manufacturing cell line for
CC expression of an anti-Rhesus D (Rhd) recombinant polyclonal antibody. An
CC anti-Rhd recombinant polyclonal antibody (A1) obtained by the method is
CC useful for the treatment, amelioration or prophylaxis in an animal. (A1)
CC is also useful for the preparation of a composition for the prophylaxis
CC of hemolytic disease of the newborn, treatment of idiopathic
CC thrombocytopenic purpura (ITP), or prevention of sensitization to the
CC Rhesus D antigen after transfusions of Rhd(+) blood to Rhd(-)
CC individuals. (A1) is useful for the diagnosis of the hemolytic diseases.
CC (M1) generates recombinant polyclonal antibody from a single cell line,
CC as a single batch, and provides a superior replacement of plasma-derived
CC prophylactic and therapeutic immunoglobulin products. The present
CC sequence represents the amino acid sequence of the light chain (LC)
CC region of an anti-Rhd Fab clone (see descriptive line for the clone
XX
XX
SQ Sequence 214 AA;
Query Match 87.5%; Score 475; DB 10; Length 214;
Best Local Similarity 87.7%; Pred. No. 2.5e-28;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYLNMYQHKRGKAPKLLIYAASLSGVP5RF 60

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DB 3 QLTQSPSSLSASVGDVNTITCRASQSSISLWYQKPGKAPKLLIYAASLSQGVPSRF 62  
QY 61 SSGSGVTDFTLTITSSLPEDFASYCOESLSASYTFCGQTKVEIKR 106  
DB 63 SSGSGTDFTLTITSSLPEDFATYYCOQSYSTPWTFCGQTKVEIKR 108

RESULT 7  
AAG93667

ID AAG93667 standard; protein; 107 AA.

AC AAG93667;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH54 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens;

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

DR MPI; 2001-388931/41.

DR N-PSDB; AAH68724.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
PT diagnostics requiring a human instead of an animal antibody and in  
PT therapeutic medicine.

PS Claim 1; Col 70; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein.  
CC preferably a human antibody, (I) having an amino acid sequence comprising  
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
CC immunostimulant activity, and can be used as an immune system stimulant.  
CC (I) can be used in diagnostics that require human antibodies instead of animal  
CC antibodies, such as determine the Rh phenotype of human red blood cells.  
CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
CC chain CDR3 amino acid sequences which are given in the exemplification of  
CC the present invention

XX SQ Sequence 107 AA;

Query Match 87.3%; Score 474; DB 4; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.6e-28;

Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVNTITCRASQSSISLWYQKPGKAPKLLIYAASLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVNTITCRASQSSISLWYQKPGKAPKLLIYAASLSQGVPSRF 61

QY 61 SSGSGVTDFTLTITSSLPEDFASYCOESLSASYTFCGQTKVEIKR 106  
DB 62 SSGSGTDFTLTITSSLPEDFATYYCOQSYSTPWTFCGQTKVEIKR 107

RESULT 8

ABO27474  
ID ABO27474 standard; protein; 107 AA.

AC ABO27474;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH54.

KW Human; RH(D) binding protein; blood typing; blood product; antibody;  
KW magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

DR MPI; 2003-512273/48.

DR N-PSDB; ACD45388.

PT New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.

PS Claim 4; Page 53; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,  
CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain

XX SQ Sequence 107 AA;

Query Match 87.3%; Score 474; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.6e-28;

Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVNTITCRASQSSISLWYQKPGKAPKLLIYAASLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVNTITCRASQSSISLWYQKPGKAPKLLIYAASLSQGVPSRF 61

QY 61 SSGSGVTDFTLTITSSLPEDFASYCOESLSASYTFCGQTKVEIKR 106  
DB 62 SSGSGTDFTLTITSSLPEDFATYYCOQSYSTPWTFCGQTKVEIKR 107

RESULT 9  
AEB74551

ID AEB74551 standard; protein; 107 AA.

AC AEB74551;

DT 23-FEB-2006 (first entry)

DE Anti-Rh(D) light chain SH54, SEQ ID 179.

KW Rh(D); erythrocyte; tissue typing; transplantation; light chain.  
KW Synthetic.

OS Synthetic.

PN US2005282252-A1.

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XX 22-DEC-2005.
PD
XX
PF 22-FEB-2005; 2005US-00064174.
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
PA (SIEG/) SIEGEL D L.
XX
PI Siegel DL;
XX
XX WPI: 2006-046435/05.
DR N-PSDB; ABE74594.
XX
XX New RH(D)-binding proteins, useful for typing donor white blood cells for
PT human leukocyte antigens for the purposes of matching donors and
PT recipients for potential transplant matching in the case of both solid
PT organ or tissue transplanting.
XX
XX Claim 5; SEQ ID NO 179; 999P; English.
PS
CC The present invention relates to novel Rh(D) antibody light and heavy
CC chains. The antibody heavy chains are given in ABE74373-ABE74400 and
CC ABE74511-ABE74525. The antibody light chains are given in ABE74398-
CC ABE74441 and ABE74526-ABE74553. The Rh(D) antigen is a red blood cell
CC membrane protein. The antibodies are useful for typing donor white blood
CC cells for human leukocyte antigen (HLA) antigens for the purposes of
CC matching donors and recipients for potential transplant matching in the
CC case of both solid (for example, kidney, heart, liver, lung) and non-
CC solid (for example, bone marrow) organ or tissue transplanting. The
CC present sequence is one such antibody light chain.
XX
SQ Sequence 107 AA;
Query Match 87.3%; Score 474; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-28;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIYNTYLNWYQHKPKAKPLLIYAASSLQSGVPSRF 60
DB 2 ELTQSPSSMSASVGDRTVITCRASQSIGTYLNWYQOKPKAKPLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYGTDFLTLLTISLQPEDFATYCCQSYSTPMTFGQGTVEIKR 106
DB 62 SSGSGGTDFLTLLTISLQPEDFATYCCQSYSTPMTFGQGTVEIKR 107

RESULT 10
AAG93663
ID AAG93663 standard; protein; 107 AA.
XX
AC AAG93663;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH49 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX OS
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 27-JUN-1997; 97US-00884045.

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PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI: 2001-388931/41.
XX N-PSDB; AAH68720.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 69; 162P; English.
PS
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (1) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
SQ Sequence 107 AA;
Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIYNTYLNWYQHKPKAKPLLIYAASSLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQSIGTYLNWYQOKPKAKPLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYGTDFLTLLTISLQPEDFATYCCQSYSTPMTFGQGTVEIKR 106
DB 62 SSGSGGTDFLTLLTISLQPEDFATYCCQSYSTPMTFGQGTVEIKR 107

RESULT 11
AAG93664
ID AAG93664 standard; protein; 107 AA.
XX
AC AAG93664;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH50 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX OS
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI: 2001-388931/41.
XX N-PSDB; AAH68721.

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XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.

XX Claim 1; Col 69; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;  
 Best Local Similarity 86.8%; Pred. No. 2.3e-28;  
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASORINTYLMVYQHKPKAPKLLIYAASLSQGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVITSCRASOSISYLMVYQKPKAPKLLIYAASLSQGVPSRF 61  
 QY 61 SSGSGYGTDFTLTITSSIQFEDFASVYCOESLSASVYTGCGTKVEIKR 106  
 DB 62 SSGSGGTDFTLTITSSIQFEDFATVYCOQSYSTPMTGCGTKVEIKR 107

#### RESULT 12

AAG93590  
 ID AAG93590 standard; protein; 107 AA.

XX AAG93590;

XX 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain I02 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KW red blood cell; Kn phenotype; diagnosis; therapeutic.

XX Homo sapiens.

XX US625455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI, 2001-388931/41.

XX N-PSDB; AAH68647.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.

XX Claim 1; Col 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein.

CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 2.3e-28;  
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASORINTYLMVYQHKPKAPKLLIYAASLSQGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDRTVITSCRASOSISYLMVYQKPKAPKLLIYAASLSQGVPSRF 61  
 QY 61 SSGSGYGTDFTLTITSSIQFEDFASVYCOESLSASVYTGCGTKVEIKR 106  
 DB 62 SSGSGGTDFTLTITSSIQFEDFATVYCOQSYSTPMTGCGTKVEIKR 107

#### RESULT 13

ABO27471  
 ID ABO27471 standard; protein; 107 AA.

XX ABO27471;

XX 12-SEP-2003 (first entry)

XX Anti-Rh(D) light chain SH50.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KW magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI, 2003-512273/48.

XX N-PSDB; ACD45385.

XX New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 52; 187pp; English.

CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;

Best Local Similarity 86.8%; Pred. No. 2.3e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVCDRTVTCRASQRIINTYLNWYQHKPKKLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVCDRTVTCRASQSISSYLNWYQHKPKKLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGDFTLTISLQFEDFPASYCOESLSASYTFQGTKEIKR 106  
DB 62 SSGSGYGDFTLTISLQFEDFPATYCCQSYSTPMTFQGTKEIKR 107

## RESULT 14

ABO27397 standard; protein; 107 AA.  
ID ABO27397  
AC ABO27397;  
XX 12-SEP-2003 (first entry)  
XX DE Anti-Rh(D) chain 102.  
XX KM Human, RH(D) binding protein; blood typing; blood product; antibody;  
XX KM magnetically activated cell sorting.  
XX OS Homo sapiens.  
XX PN US2003040605-A1.  
XX PD 27-FEB-2003.  
XX PF 04-MAY-2001; 2001US-00848798.  
XX PR 11-OCT-1996; 96US-0028550P.  
XX PR 27-JUN-1997; 97US-00884045.  
XX PR 10-APR-1998; 98US-0081380P.  
XX PR 29-JAN-1999; 99US-00240274.  
XX PA (UYPE-) UNIV PENNSYLVANIA.  
XX PI Siegel DL;  
XX DR WPI; 2003-512273/48.  
XX DR N-PSDB; ACD45311.  
XX PT New human Rh(D)-binding protein useful for various diagnostic and  
XX PT therapeutic applications, including typing of blood or blood products.  
XX PS Claim 4; Page 26; 187pp; English.  
XX CC The invention relates to an isolated Rh(D) binding protein. The protein  
XX CC can be used for magnetically activated cell sorting. The protein is  
XX CC useful in various diagnostic and therapeutic applications in humans,  
XX CC including typing of blood or blood products. The present sequence  
XX CC represents the amino acid sequence of a human anti-Rh(D) chain  
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 2.3e-28;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVCDRTVTCRASQRIINTYLNWYQHKPKKLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVCDRTVTCRASQSISSYLNWYQHKPKKLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGDFTLTISLQFEDFPASYCOESLSASYTFQGTKEIKR 106  
DB 62 SSGSGYGDFTLTISLQFEDFPATYCCQSYSTPMTFQGTKEIKR 107

RESULT 15  
ABO27470

ID ABO27470 standard; protein; 107 AA.

XX ABO27470;  
XX AC ABO27470;  
XX XX 12-SEP-2003 (first entry)  
XX DE Anti-Rh(D) light chain SH49.  
XX KM Human, RH(D) binding protein; blood typing; blood product; antibody;  
XX KM magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2003-512273/48.

XX N-PSDB; ACD45384.

XX New human Rh(D)-binding protein useful for various diagnostic and

XX PT therapeutic applications, including typing of blood or blood products.

XX PS Claim 4; Page 52; 187pp; English.

XX CC The invention relates to an isolated Rh(D) binding protein. The protein

XX CC can be used for magnetically activated cell sorting. The protein is

XX CC useful in various diagnostic and therapeutic applications in humans,

XX CC including typing of blood or blood products. The present sequence

XX CC represents the amino acid sequence of a human anti-Rh(D) chain

XX SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.3e-28;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVCDRTVTCRASQRIINTYLNWYQHKPKKLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVCDRTVTCRASQSISSYLNWYQHKPKKLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGDFTLTISLQFEDFPASYCOESLSASYTFQGTKEIKR 106  
DB 62 SSGSGYGDFTLTISLQFEDFPATYCCQSYSTPMTFQGTKEIKR 107

Search completed: August 30, 2006, 00:41:52  
Job time : 96.2394 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 9.95758 Seconds  
(without alignments)  
1024.243 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDVTVIS.....QESLSASVYGGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR 80:\*  
2: p1r1:\*  
3: p1r2:\*  
4: p1r3:\*  
5: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	464	85.5	127	2	S40367 Ig kappa chain V-J
2	459	84.5	123	2	S40331 Ig kappa chain - h
3	458	84.3	108	2	B49047 Ig kappa chain V r
4	456	84.0	108	2	S47182 Ig kappa chain - h
5	452	83.2	109	2	S31998 Ig kappa chain - h
6	452	83.2	109	2	S31979 Ig kappa chain - h
7	448	82.5	109	2	S31980 Ig kappa chain - h
8	446	82.1	108	2	S44122 Ig kappa chain V r
9	445	82.0	109	2	S32001 Ig kappa chain - h
10	441	81.2	108	2	S19674 Ig kappa chain V r
11	439	80.8	109	2	S31981 Ig kappa chain - h
12	439	80.8	129	2	S52793 Ig kappa chain V r
13	438	80.7	107	2	S36264 Ig lambda chain V
14	437	80.5	108	2	S31977 Ig kappa chain - h
15	436	80.3	109	2	S31983 Ig kappa chain - h
16	436	80.3	122	2	S40370 Ig kappa chain - h
17	436	80.3	129	1	K1HUKK Ig kappa chain pre
18	436	80.3	129	1	S40317 Ig kappa chain - h
19	435	80.1	128	2	S46372 Ig light chain var
20	434	79.9	120	2	S46370 Ig kappa chain V-J
21	433	79.8	105	2	S40315 Ig kappa chain - h
22	433	79.7	108	1	K1HUKK Ig kappa chain V-I
23	432	79.6	132	2	S40334 Ig kappa chain - h
24	431	79.4	109	2	S31978 Ig kappa chain - h
25	430	79.2	108	1	K1HUKK Ig kappa chain V-I
26	430	79.2	132	2	S38646 Ig kappa chain V r
27	425	78.3	122	2	S40314 Ig kappa chain - h
28	425	78.3	129	2	S40369 Ig kappa chain - h
29	424.5	78.2	106	2	PC2397 anti-tetanus toxin

30	423.5	78.0	124	2	S40336 Ig kappa chain V-J
31	422.5	77.8	107	2	S36275 Ig lambda chain V
32	422	77.7	125	2	S40333 Ig kappa chain V-J
33	422	77.7	131	2	S40352 Ig kappa chain V-J
34	420	77.3	108	1	K1HUKK Ig kappa chain V-I
35	420	77.3	125	2	S40349 Ig kappa chain V-J
36	420	77.3	126	2	S40335 Ig kappa chain V-J
37	419	77.2	125	2	S40350 Ig kappa chain - h
38	418	77.0	117	2	S46371 Ig kappa chain V r
39	418	77.0	129	2	S52792 Ig kappa chain V r
40	417	76.8	117	2	S46376 Ig kappa chain V-J
41	416	76.6	108	1	K1HUKK Ig kappa chain V-I
42	414	76.2	107	2	JL0139 Ig kappa chain V r
43	414	76.2	107	2	S36262 Ig kappa chain V r
44	414	76.2	108	1	K1HUKK Ig kappa chain V-I
45	413.5	76.2	108	2	S30521 Ig kappa chain V r

#### ALIGNMENTS

RESULT 1  
S40367  
Ig kappa chain V-J-C region - human  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40367  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MVID:94080891; PMID:8258341  
A/Accession: S40367  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-127 <KLE>  
A/Cross-references: UNIPARC:DP10000176CB4; EMBL:X72477  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 464; DB 2; Length 127;  
Best Local Similarity 84.9%; Pred. No. 2,6e-34;  
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDVTVISCRASORINTYLNYYOHKPKAPLTLTYAASSLQGVPSRF 60  
DB 20 QMTQSPSSLSASVGVDRVITLCRASQISINLYNMYOKPKAPLTLTYAASSLQGVPSRF 79  
QY 61 SSGSGYTDFTLTITSSIQPEDFASVYCCESLSASVYFGQGTKEIKR 106  
DB 80 SSGSGYTDFTLTITSSIQPEDFASVYCCESLSASVYFGQGTKEIKR 125

RESULT 2  
S40331  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40331  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MVID:94080891; PMID:8258341  
A/Accession: S40331  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-123 <KLE>  
A/Cross-references: UNIPARC:DP100001161S1; EMBL:X72441; MVID:9441350; PIDD:CAA51109.1; PII  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/32-106/Domain: immunoglobulin homology <IMM>  
Query Match 84.5%; Score 459; DB 2; Length 123;



C/Accession: S31980; S32000  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C/Accession: S31981  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 submitted to the EMBL Data Library, June 1992  
 C/Keywords: heterotrimer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 448; DB 2; Length 109;  
 Best Local Similarity 81.0%; Pred. No. 5.9e-33;  
 Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASLSLQSGVPSRFS 61  
 :|||||  
 DB 4 MTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYGTSLQSGVPSRFS 63  
 :|||||  
 QY 62 GSGYGDTFTLTISLQFEDFASYYCOESLSASVTFGQGTKEIKR 106  
 :|||||  
 DB 64 GSGGTFDTLTISLQFEDFATYFCQOYSSTPYTFGQGTKEIKR 108  
 :|||||

# RESULT 8

S34122  
 Ig kappa chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
 C/Accession: S44122  
 R/Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
 submitted to the EMBL Data Library, March 1994  
 A/Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable  
 A/Reference number: S44105  
 A/Accession: S44122  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-108 <HAM>  
 A/Cross-references: UNIPARC:UPI0000116630; EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PID  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 446; DB 2; Length 108;  
 Best Local Similarity 83.0%; Pred. No. 8.7e-33;  
 Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASLSLQSGVPSRFS 60  
 :|||||  
 DB 3 QMTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYASLSLQSGVPSRFS 62  
 :|||||  
 QY 61 GSGYGDTFTLTISLQFEDFASYYCOESLSASVTFGQGTKEIKR 106  
 :|||||  
 DB 63 GSGGTFDTLTISLQFEDFATYFCQOYSSTPYTFGQGTKEIKR 108  
 :|||||

# RESULT 9

S32001  
 Ig kappa chain - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C/Accession: S32001  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
 A/Reference number: S31977  
 A/Accession: S32001  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-109 <POR>

A/Cross-references: UNIPARC:UPI0000116498; EMBL:Z15082; NID:938503; PIDN:CAA78791.1; PID  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 445; DB 2; Length 109;  
 Best Local Similarity 80.0%; Pred. No. 1.1e-32;  
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASLSLQSGVPSRFS 61  
 :|||||  
 DB 4 MTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYGTSLQSGVPSRFS 63  
 :|||||  
 QY 62 GSGYGDTFTLTISLQFEDFASYYCOESLSASVTFGQGTKEIKR 106  
 :|||||  
 DB 64 GSGGTFDTLTISLQFEDFATYFCQOYSSTPYTFGQGTKEIKR 108  
 :|||||

# RESULT 10

S19674  
 Ig kappa chain V region (clone alpha-Tel9) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
 C/Accession: S19674  
 R/Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.  
 Mol. Biol. 222, 581-597, 1991  
 A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph  
 A/Reference number: S19663; NID:92085276; PMID:1748994  
 A/Accession: S19674  
 A/Molecule type: mRNA  
 A/Residues: 1-108 <MAR>  
 A/Cross-references: UNIPARC:UPI0000115F81; EMBL:X61642; NID:937860; PIDN:CAA43823.1; PID  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 441; DB 2; Length 108;  
 Best Local Similarity 82.9%; Pred. No. 2.4e-32;  
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASLSLQSGVPSRFS 61  
 :|||||  
 DB 4 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASLSLQSGVPSRFS 63  
 :|||||  
 QY 62 GSGYGDTFTLTISLQFEDFASYYCOESLSASVTFGQGTKEIKR 106  
 :|||||  
 DB 64 GSGGTFDTLTISLQFEDFATYFCQOYSSTPYTFGQGTKEIKR 108  
 :|||||

# RESULT 11

S31981  
 Ig kappa chain - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S31981  
 R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
 A/Reference number: S31977  
 A/Accession: S31981  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-109 <POR>  
 A/Cross-references: UNIPARC:UPI0000116494; EMBL:Z15077; NID:938493; PIDN:CAA78786.1; PID  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;  
 Best Local Similarity 80.0%; Pred. No. 3.7e-32;  
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKGKAPKLLIYAASLSLQSGVPSRFS 61

Db 4 MTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 63

Qy 62 GSGGYGTDFTLTITSSLOPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 Db 64 GSGSGTDFTLTITSSLOPEDFATYTCQOSYSTPTFGQGTLEIKR 108

## RESULT 12

S52793

Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000

C/Accession: S52793

R/Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995

A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-

A/Reference number: S52789

A/Accession: S52793

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-129 &lt;ROC&gt;

A/Cross-references: UNIPARC:UPI0000116222; EMBL:X85997; NID:9758600; PIDN:CAA59989.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.8%; Score 439; DB 2; Length 129;  
 Best Local Similarity 81.9%; Pred. No. 4.3e-32;

Matches 86; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRF 60  
 Db 25 QMTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRF 84

Qy 61 GSGGYGTDFTLTITSSLOPEDFASYYCOESLSASYTFGQGTVEIKR 105  
 Db 85 VGSAGTDFTLTITSSLOPEDFATYTCQOSYSTPTFGQGTVEIKR 129

## RESULT 13

S36264

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C/Accession: S36264

R/Gilfith, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MUID:93178448; PMID:7679990

A/Accession: S36264

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-107 &lt;GRI&gt;

A/Cross-references: UNIPARC:UPI0000118DF4; EMBL:Z18845; NID:933426; PIDN:CAA79297.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.7%; Score 438; DB 2; Length 107;  
 Best Local Similarity 83.7%; Pred. No. 4.4e-32;  
 Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 61  
 Db 4 LTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 63

Qy 62 GSGGYGTDFTLTITSSLOPEDFASYYCOESLSASYTFGQGTVEIKR 105  
 Db 64 GSGSGTDFTLTITSSLOPEDFATYTCQOSYSTPTFGQGTVEIKR 107

## RESULT 14

S31977  
 Ig kappa chain - human  
 C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C/Accession: S31977

R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31977

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 &lt;POR&gt;

A/Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176B27; EMBL:Z15073

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.5%; Score 437; DB 2; Length 108;  
 Best Local Similarity 82.9%; Pred. No. 5.5e-32;  
 Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 61  
 Db 4 MTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 63

Qy 62 GSGGYGTDFTLTITSSLOPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 Db 64 GSGSGTDFTLTITSSLOPEDFATYTCQOSYSTPTFGQGTVEIKR 108

## RESULT 15

S31983

Ig kappa chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S31983

R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL Data Library, June 1992

A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A/Reference number: S31977

A/Accession: S31983

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 &lt;POR&gt;

A/Cross-references: UNIPARC:UPI0000116496; EMBL:Z15079; NID:938497; PIDN:CAA78788.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.3%; Score 436; DB 2; Length 109;  
 Best Local Similarity 79.0%; Pred. No. 6.8e-32;  
 Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 61  
 Db 4 MTQSPSSLSASVGDRTYITTCRASQDISRYLNMWYQKRGKAPKLLIYAASSLQSGVPSRFS 63

Qy 62 GSGGYGTDFTLTITSSLOPEDFASYYCOESLSASYTFGQGTVEIKR 106  
 Db 64 GSGSGTDFTLTITSSLOPEDFATYTCQOSYSTPTFGQGTVEIKR 108

Search completed: August 30, 2006, 00:42:55  
 Job time : 10.9576 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 57.8182 Seconds

(without alignments)  
1695.862 Million cell updates/sec

Title: US-10-027-725a-10

Perfect score: 543

Sequence: 1 ERLQSPSSLSASVGDRTIS.....QESLSASYTGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	85.6	108	2	Q9UL77_HUMAN
2	449.5	82.8	107	2	Q96SAS_HUMAN
3	439.5	80.9	107	2	Q9UL81_HUMAN
4	439	80.8	236	2	Q6GMX0_HUMAN
5	436	80.3	129	1	KV1W_HUMAN
6	436	80.3	236	2	Q6GMX8_HUMAN
7	434	79.9	236	2	Q6GMW1_HUMAN
8	433	79.7	108	1	KV1E_HUMAN
9	430	79.2	108	1	KV1H_HUMAN
10	424	78.1	236	2	Q6PIH7_HUMAN
11	422	77.7	108	2	Q9UL79_HUMAN
12	420	77.3	108	1	KV1N_HUMAN
13	420	77.3	108	2	Q9UL70_HUMAN
14	418	77.0	234	2	Q7Z473_HUMAN
15	416	76.6	108	1	KV1F_HUMAN
16	414	76.2	108	1	KV1K_HUMAN
17	413	76.1	108	1	KV1V_HUMAN
18	412	75.9	108	1	KV1O_HUMAN
19	412	75.9	236	2	Q7Z3Y4_HUMAN
20	411	75.7	236	2	Q5O2W4_HUMAN
21	409	75.3	108	1	KV1G_HUMAN
22	408	75.1	108	1	KV1M_HUMAN
23	407	75.0	108	1	KV1B_HUMAN
24	406	74.8	108	1	KV1R_HUMAN
25	406	74.8	234	2	Q5EEF6_HUMAN
26	404	74.4	108	1	KV1A_HUMAN
27	404	74.4	189	2	Q5G9I7_HUMAN
28	400	73.7	236	2	Q6PIH4_HUMAN
29	399.5	73.6	107	1	KV1D_HUMAN
30	399	73.5	108	1	KV1S_HUMAN
31	398	73.3	108	1	KV1P_HUMAN

32	397	73.1	108	1	KV1L_HUMAN	P01604 homo sapien
33	397	73.1	129	1	KV1X_HUMAN	P04432 homo sapien
34	397	73.1	236	2	Q6GMX9_HUMAN	Q6GMX9 homo sapien
35	396	72.9	108	1	KV1J_HUMAN	P80362 homo sapien
36	396	72.9	236	2	Q6PIF5_HUMAN	Q6PIF5 homo sapien
37	394	72.6	244	2	Q6S2C8_HUMAN	Q6S2C8 homo sapien
38	391	72.0	108	1	KV1O_HUMAN	P01609 homo sapien
39	391	72.0	240	2	Q6S2C9_HUMAN	Q6S2C9 homo sapien
40	385.5	71.3	109	1	KV1T_HUMAN	P01612 homo sapien
41	384	70.7	108	1	KV1C_HUMAN	P01595 homo sapien
42	376	69.2	108	1	KV5T_MOUSE	P01653 mus musculu
43	373	68.7	108	1	KV5S_MOUSE	P01652 mus musculu
44	371	68.3	108	2	Q9UL83_HUMAN	Q9UL83 homo sapien
45	371	68.3	116	2	Q96PF6_HUMAN	Q96PF6 homo sapien

#### ALIGNMENTS

RESULT 1  
Q9UL77\_HUMAN PRELIMINARY; PRT; 108 AA.  
AC Q9UL77;  
DT 01-MAY-2000, integrated into UniProtKB/TREMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98271719; PubMed=9614934; DOI=10.1006/cclin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92387224; PubMed=1516616;  
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
RT "Human monoclonal striational autoantibodies isolated from thymic B  
RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
RT segments associated with the autoimmune repertoire";  
RL Eur. J. Immunol. 22:2231-2236(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93170387; PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
RT distributed over a large portion of the V kappa locus and do not show  
RT somatic mutation";  
RL Eur. J. Immunol. 23:391-397(1993).  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC EMBL: AF035037; AAC56273.1; -; mRNA.  
CC PIR: B49047; B49047.  
CC PIR: S34083; S34083.  
CC HSSP: P01607; IBMW.  
CC SMR: Q9UL77; 1-108.  
CC Ensembl: ENSG00000163245; Homo sapiens.  
CC InterPro: IPR003599; IG.  
CC InterPro: IPR007110; IG-like.  
CC InterPro: IPR003596; IG\_v.  
CC InterPro: IPR013106; V-set.  
CC SMART: SM00409; IG; 1.  
CC SMART: SM00406; IGv; 1.  
CC PROSITE: PSS0835; IG\_LIKE; 1.



KM Immunoglobulin domain.  
 FT NON\_TER 1  
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;  
 Query Match 85.6%; Score 465; DB 2; Length 108;  
 Best Local Similarity 84.9%; Pred. No. 7.2e-42;  
 Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTISCRASQRIINTYLMYQHKGKAPKLLIYAASSLSQSVSRF 60  
 DB 3 QMTQSPSSLSASVGDRTTITCRASQSISSYLMYQOKPGKAPKLLIYAASSLSQSVSRF 62  
 QY 61 SSGSGYGFDTLTISLQFEDFASYSYCOESLSASYSYFGQGTKEIKR 106  
 DB 63 SSGSGSGDTFTLTISLQPEDFATYCCQQSISTSTMTFEGTKVEIKR 108

RESULT 2  
 ID Q96SA9\_HUMAN PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9; 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 18.  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes";  
 RL Eur. J. Immunol. 16:12020-2031(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92387224; PubMed=1516616;  
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
 RT "Human monoclonal strictional autoantibodies isolated from thymic B  
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
 RT segments associated with the autoimmune repertoire";  
 RL Eur. J. Immunol. 22:2231-2236(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93170387; PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;  
 RA Mahneimer-Loty A., Katz J.B., Pillingner M., Gnossein C., Smith A.,  
 RT "Molecular characteristics of antibodies bearing an anti-DNA-  
 RT associated idiotype";  
 RL Eur. Med. 174:1639-1652(1991).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91243737; PubMed=1903706;  
 RA Blaison G., Kuntz J.L., Pasquali J.L.;  
 RT "Molecular analysis of V kappa III variable regions of polyclonal  
 RT rheumatoid factors during rheumatoid arthritis";  
 RL Eur. J. Immunol. 21:1221-1227(1991).  
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 CC -----  
 DR EMBL: U96396; AAB68785.1; -, mRNA.  
 DR PIR: B49047; B49047.  
 DR PIR: PH0867; PH0867.  
 DR PIR: S16840; S16840.  
 DR PIR: S31977; S31977.  
 DR PIR: S34083; S34083.  
 DR PIR: S34086; S34086.  
 DR HSSP: P01607; 1BMW.  
 DR SMR: Q96SA9; 1-107.  
 DR Ensemble: ENSG00000163245; Homo sapiens.  
 DR LinkHub; Q96SA9; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003596; IG\_v.  
 DR InterPro: IPR013106; V-set.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin domain.  
 FT NON\_TER 1  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;  
 Query Match 82.8%; Score 449.5; DB 2; Length 107;  
 Best Local Similarity 84.9%; Pred. No. 3.3e-40;  
 Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTTISCRASQRIINTYLMYQHKGKAPKLLIYAASSLSQSVSRF 60  
 DB 3 QMTQSPSSLSASVGDRTTITCRASQSISSYLMYQOKPGKAPKLLIYAASSLSQSVSRF 62  
 QY 61 SSGSGYGFDTLTISLQFEDFASYSYCOESLSASYSYFGQGTKEIKR 106  
 DB 63 SSGSGSGDTFTLTISLQPEDFATYCCQQSISTSTMTFEGTKVEIKR 107

RESULT 3  
 ID Q9UL81\_HUMAN PRELIMINARY; PRT; 107 AA.  
 AC Q9UL81;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 21.  
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
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 CC -----  
 DR EMBL: AF035033; AAD56269.1; -, mRNA.  
 DR HSSP: P01607; 1BMW.  
 DR SMR: Q9UL81; 1-107.  
 DR LinkHub; Q9UL81; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003596; IG\_v.  
 DR InterPro: IPR013106; V-set.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00406; IGv; 1.



DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549PDE0754748 CRC64;  
Query Match 80.9%; Score 439.5; DB 2; Length 107;  
Best Local Similarity 82.1%; Pred. No. 3.9e-39;  
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;  
QY 1 ELTQSPSSLSASVGDGVITTCRASQRIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 3 QMTQSPSSLSASVGDGVITTCRASQSIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 62  
QY 61 SSGSGYDTFTLTITSSLPQEDFASYYCOESLSASVTFGGQTKVEIKR 106  
DB 63 SSGSGYDTFTLTITSSLPQEDFASYYCOESLSASVTFGGQTKVEIKR 107  
RESULT 4  
OG6MX0\_HUMAN PRELIMINARY; PRT; 236 AA.  
ID OG6MX0;  
AC OG6MX0;  
DT 19-JUL-2004, integrated into UniProtKB/TREMBL.  
DT 19-JUL-2004, sequence version 1.  
DE 07-FEB-2006, entry version 16.  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,  
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzyzanski M.I., Skalska U., Smilans D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; BC073775; AAH7375.1; -, mRNA.  
DR SMR; Q6GMX0; 23-236.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.

DR InterPro; IPR03306; V-set.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00407; IG\_C1; 1.  
DR SMART; SM00406; IG\_V; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E928BF8 CRC64;  
Query Match 80.8%; Score 439; DB 2; Length 236;  
Best Local Similarity 81.1%; Pred. No. 1.1e-38;  
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDGVITTCRASQRIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 25 QMTQSPSSLSASVGDGVITTCRASQRIINLYLMYQHKPKAPKLLIYAASSLSQGVPSRF 84  
QY 61 SSGSGYDTFTLTITSSLPQEDFASYYCOESLSASVTFGGQTKVEIKR 106  
DB 85 SSGSGYDTFTLTITSSLPQEDFASYYCOESLSASVTFGGQTKVEIKR 130  
RESULT 5  
KV1W\_HUMAN STANDARD; PRT; 129 AA.  
ID KV1W\_HUMAN  
AC P04431;  
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.  
DT 13-AUG-1987, sequence version 1.  
DE 07-MAR-2006, entry version 39.  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobbeck H.G., Combrist G., Zachau H.G.,  
RT "Immunoglobulin genes of the kappa light chain type from two human  
lymphoid cell lines are closely related.";  
RL Nucleic Acids Res. 12:6995-7006(1984).  
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CC EMBL; X00965; CAA25477.1; ALT\_TERM; Genomic DNA.  
CC PIR; A01883; K1HWK.  
DR HSSP; P01607; 1BWV.  
DR SMR; P04431; 23-129.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR InterPro; IPR03306; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00406; IG; 1.  
DR SMART; SM00409; IG\_V; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1  
FT CHAIN 23  
FT REGION 23 45 Ig kappa chain V-I region Walker.  
FT REGION 46 56 Framework-1.  
FT REGION 57 71 Complementarity-determining-1.  
FT REGION 72 78 Framework-2.  
FT REGION 79 110 Complementarity-determining-2.  
FT REGION 111 119 Framework-3.  
FT Complementarity-determining-3.

FT	REGION	120	129	Framework-4.
FT	DISUPID	45	110	By similarity.
FT	NON_TER	129	129	
SO	SEQUENCE	129 AA;	14069 MM;	F941FA07D4AFC2F9 CRC64;
Query Match				
Best Local Similarity		80.3%;	Score 436;	DB 1; Length 129;
Matches	86;	Conservative	8;	Mismatches 11; Indels 0; Gaps 0;
Oy	1	ELTQSPSSLSASVGRNVITSCASGRINITYLNWQHKKGKAPKLIIVAASSLQSGVPRF	60	
Db	25	QMTQSPSSLSASVGRVITTCASQISISYLNWYQKQKAPKLIIVAASSLQSGVTSRF	84	
Oy	61	SGSGGDTFTLTLSLQFEDFASVYCOESLSASYTFGGQTKVEIK	105	
Db	85	SGSGGDTFTLTLSLQPEDSASTYCCQGSYSLTIFGGQTRERIK	129	
RESULT 6				
O6GMX8 HUMAN				
ID	O6GMX8 HUMAN	PRELIMINARY;	PRT;	236 AA.
AC	O6GMX8			
DT	19-JUL-2004	integrated into UniProtKB/TrEMBL.		
DT	19-JUL-2004	sequence version 1.		
DT	07-FEB-2006	entry version 17.		
DE	IGKC protein.			
GN	Name=IGKC;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homnidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
ON	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strasberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,			
RA	Altchul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Quagliano N.A., Peters G.J., Abramson R.D., Miliady S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.U., Malek U.A., Gunaratne P.H.,			
RA	Villarino S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Richardson D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,			
RA	Genersch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RC	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Primary B-Cells;			
RL	NIH MGC Project;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
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CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL; BC073764; AAH73764.1; -; mRNA.			
DR	SMR; O6GMX8; 24-235.			
DR	Ensembl; ENSG00000163245; Homo sapiens.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003597; IG_cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			

DR	InterPro:IPR013106; V-set.
DR	Pfam: PF07654; C1-sec; 1.
DR	SMART: SM00409; IG; 1.
DR	SMART: SM00407; IGCL; 1.
DR	SMART: SM00406; IGY; 1.
DR	PROSITE; PSS0835; IG_LIKE; 2.
DR	PROSITE; PSS00290; IG_MHC; UNKNOWN; 1.
SQ	SEQUENCE 236 AA; 25707 MW; 4fCBEL1AB6559EFC9 CRC64;
Query March	80.3%; Score 436; DB 2; Length 236;
Best Local Similarity	80.2%; Pred. No. 2,3e-38;
Matches 85; Conservative 12; Mismatches 9; Indels 0; Gaps	
Oy	1 ELTQPSSLSASVGDVRTISCRASQRINTYLMWYGHKPGKAPKLTLIYAASSLQSGVPSPF 60
Dd	25 QMTQPSFSVASVDRTVTTCRASOGSISSLAWYQQKPKGAPKLTLLIYAASSLQSGVSRF 84
Oy	61 SGGSYGDFLTITSLIQEDFAFYCOESLSASYTGCGKYIKR 106
Dd	85 SGSSGTFDLTITSLIQEDFAFYCOQHSPFPFTGPGTKIDIKR 130
RESULT 7	
OG6GMW1_HUMAN	
ID	OG6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC	OG6GMW1;
DT	19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT	19-JUL-2004, sequence version 1.
DE	07-FEB-2006, entry version 17.
DE	IGKC protein.
GN	Name=IGKC;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Spleen;
EX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Klausner R.D., Collins F.S., Wagner L.H., Shennan C.M., Schuler G.D.,
RA	Aleschul S.F., Zeeberg B., Batzer K.H., Schaefer C.F., Heich F.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA	Ditschenko L., Mansina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton W., Soares M.B., Bonaldo M.F., Cassavari P., Prange C.,
RA	Brownstein M.J., Ustin T., Yoshiyuki S., Carninci P., Abrahams R.D., Mullany S.J.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.L., Gay L.U., Hulik S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Shevchenko Y., Bouffard G.G.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Dickinson M.C.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Butterfield J.S.N., Kirzyanski M.I., Skalska U., Smielus D.E.,
RA	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Spleen;
RG	NIH MGC Project;
RU	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC	Copied by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	EMBL; BC073791; AAH73791.1; - mRNA.
DR	SMR; OG6GMW1; 24-236.
DR	Ensembl; ENSG00000163245; Homo sapiens.
DR	InterPro; IPR003599; IG.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003066; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR SQUONCE 236 AA; 25751 MW; 5BFE6A087APAC437 CRC64;  
SQ

Query Match 79.9%; Score 434; DB 2; Length 236;  
Best Local Similarity 81.1%; Pred. No. 3, 8e-38;  
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 25 QMTQSPSSLSASVGDRTVITCRASQGISNDLGWYQKPGKAPKLLIYAASSLSQGVPSRF 84

QY 61 SGSGYGDFLTLTSSLOFEDFPASYCOESLSASTFGQGTKEIKR 106  
Db 85 SGSGSGTDFLTLTSSLOFEDFPATYYCLQDYNYPWTFGQGTKEIKR 130

RESULT 8  
KVLE\_HUMAN STANDARD; PRT; 108 AA.  
ID PO1597;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 21-JUL-1986, sequence version 1.  
DT 07-MAR-2006, entry version 39.  
DE Ig kappa chain V-I region DEE.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=7205133; PubMed=5124396;  
RA Milstein C.P., Deveron E.V.;  
RT "The amino acid sequence of a human kappa light chain.";  
RL Biochem J 123:945-958(1971).  
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
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CC PIR; A01865; K1HUUDE.  
DR HSSP; PO1607; 1BMW.  
DR SMR; PO1597; 4-108.  
DR GO; GO:0005576; C:extracellular region; NMS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
DR Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
KW CHAIN 1  
FT 1 >108  
FT REGION 1 23 Ig kappa chain V-I region DEE.  
FT REGION 24 34 Framework-1.  
FT REGION 35 49 Complementarity-determining-1.  
FT REGION 50 56 Framework-2.  
FT REGION 57 88 Complementarity-determining-2.  
FT REGION 88 Framework-3.

FT REGION 89 97 Complementarity-determining-3.  
FT REGION 98 107 Framework-4.  
FT DISUPFID 23 88 By similarity.  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1B51 CRC64;  
SQ

Query Match 79.7%; Score 433; DB 1; Length 108;  
Best Local Similarity 77.4%; Pred. No. 2e-38;  
Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 3 ZMTQSPSSLSASVGDRTVITCRAGQSVNRYLMYQKPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGDFLTLTSSLOFEDFPASYCOESLSASTFGQGTKEIKR 106  
Db 63 SGSGSGTDFLTLTSSLOFEDFPATYYCQDYNYPWTFGQGTKEIKR 108

RESULT 9  
KVLE\_HUMAN STANDARD; PRT; 108 AA.  
ID PO1600;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 21-JUL-1986, sequence version 1.  
DT 07-MAR-2006, entry version 44.  
DE Ig kappa chain V-I region Hau.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=71032830; PubMed=4097974;  
RA Watanabe S., Hilschmann N.;  
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
RT chain of subgroup I (Bence-Jones protein Hau): subdivision within  
RT subgroups.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivative License  
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CC PIR; A01868; K1HUUH.  
DR PDB; 1F6L; X-ray; L=1-89.  
DR GO; GO:0005576; C:extracellular region; NMS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG-LIKE; 1.  
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin domain; Immunoglobulin V region.  
KW CHAIN 1  
FT 1 >108  
FT REGION 1 23 Framework-1.  
FT REGION 24 34 Complementarity-determining-1.  
FT REGION 35 49 Framework-2.  
FT REGION 50 56 Complementarity-determining-2.  
FT REGION 57 88 Framework-3.  
FT REGION 89 97 Complementarity-determining-3.  
FT REGION 98 107 Framework-4.  
FT DISUPFID 23 88 By similarity.  
FT NON\_TER 108 108  
FT STRAND 4 7

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FT STRAND 9 12
FT TURN 15 16
FT STRAND 19 27
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT STRAND 77 77
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 92 95
FT STRAND 98 98
FT STRAND 102 105
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160BD9D0618 CRC64;

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Query Match 79.2%; Score 430; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 4.2e-38;
Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

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Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITSCRASQSISSYLSWYQKPKAPKLLIYAASSLSQGVPSRF 62
Qy 61 SSGSGYGTDFLTITSSIQFEDFPASYCOESLSASYTFGQGTKEIKR 106
Db 63 SSGSGGTDFLTITSSIQFEDFPATYCCQNYITPTSPFGGTFVEIKR 108

```

## RESULT 10

Q6PIH7\_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH7; Integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 17.

DE IGKC protein.

GN Name=IGKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI\_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=lung;

RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci F., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; IAR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

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Query Match 78.1%; Score 424; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 4.5e-37;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

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Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 25 QLTQSPSSLSASVGDRTVITSCRASQSISSYLSWYQKPKAPKLLIYAASSLSQGVPSRF 84
Qy 61 SSGSGYGTDFLTITSSIQFEDFPASYCOESLSASYTFGQGTKEIKR 106
Db 85 SSGSGGTDFLTITSSIQFEDFPATYCCQNLNSPPTFGGTFVEIKR 130

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## RESULT 11

Q9UL79\_HUMAN PRELIMINARY; PRT; 108 AA.

AC Q9UL79; Integrated into UniProtKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 21.

DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI\_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=9827119; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,

RA Young D.C.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

RN NUCLEOTIDE SEQUENCE.

RX MEDLINE=92289816; PubMed=1601042;

RA Huber C., Klobbeck H.G., Zachau H.G.,

RT "Ongoing V kappa-J kappa recombination after formation of a productive

RT V kappa-J kappa coding joint."

RL Eur. J. Immunol. 22:1561-1565(1992).

RN NUCLEOTIDE SEQUENCE.

RX MEDLINE=93170387; PubMed=8436174;

RA Wagner S.D., Luzzatto L.,

RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are

RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation."  
 RL Eur. J. Immunol. 23:391-397(1993).  
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 CC -----  
 CC EMBL: AF035035; AAD56271.1; -; mRNA.  
 DR PIR: S23638; S23638.  
 DR PIR: S30521; S30521.  
 DR PIR: S34090; S34090.  
 DR HSSP: P01607; 1BMW.  
 DR SMR: Q9UL79; 1-108.  
 DR LinkHub: Q9UL79; -.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR SMART: SM00409; Ig; 1.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin domain.  
 FT NON\_TER 1 1  
 FT SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;  
 SQ  
 Query Match 77.7%; Score 422; DB 2; Length 108;  
 Best Local Similarity 80.0%; Pred. No. 3e-37;  
 Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;  
 QY 2 LTQSPSSLSASVGDVITISCRASQRIINTYLNMYOHKPKAPKLLIYAASLSQGVPSRF 61  
 Db 4 MTQSPSLASSTGDRVITISCRMSGSGISYLAWYQKKGKAPPELLIYAASLTQGVPSRF 63  
 QY 62 GSGYGIDFTLTITSLQFDPASVYCOESLSASTFGGKTVEIKR 106  
 Db 64 GSGSGIDFTLTITSLQFDPATYCCQYSPFPFGGKTVEIKR 108  
 RESULT 12  
 ID KVIN\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01606;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 07-MAR-2006, entry version 39.  
 DE Ig kappa chain V-I region OU.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=70201507; PubMed=5447531;  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;  
 RT "Macroglobulin structure: variable sequence of light and heavy  
 RT chains".  
 RL Science 169:56-59(1970).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
 CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's  
 CC macroglobulin.  
 CC -----  
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 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC -----  
 CC PIR: A01872; KIHUOU.  
 DR HSSP: P01607; 1BMW.  
 DR LinkHub: P01606; -.  
 DR GO: GO:0005576; C:extracellular region; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR003599; Ig.

DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig V.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07686; V-set; 1.  
 DR SMART: SM00409; Ig; 1.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Direct protein sequencing; Immunoglobulin domain;  
 KM Immunoglobulin V region.  
 FT CHAIN 1 >108  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11779 MW; 8283DA24105827E CRC64;  
 Query Match 77.3%; Score 420; DB 1; Length 108;  
 Best Local Similarity 68.9%; Pred. No. 5e-37;  
 Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNMYOHKPKAPKLLIYAASLSQGVPSRF 60  
 Db 3 QMTZSSSSLSASVGBVITITCRASZTISYLBMYZZKPKGAPPELLIYAASBLHSGVPSRF 62  
 QY 61 GSGYGIDFTLTITSLQFDPASVYCOESLSASTFGGKTVEIKR 106  
 Db 63 GSGSGIDFTLTITSLQFDPATYCCZSYSPFTTGZGRLZIKR 108  
 RESULT 13  
 ID Q9UL70\_HUMAN PRELIMINARY; PRT; 108 AA.  
 AC Q9UL70;  
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 22.  
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus".  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;  
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosesein C., Smith A.,  
 RA Diamond B.;  
 RT "Molecular characteristics of antibodies bearing an anti-DNA-  
 RT associated idiotype".  
 RL J. Exp. Med. 174:1639-1652(1991).  
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 CC -----  
 CC EMBL: AF035044; AAD56280.1; -; mRNA.  
 DR PIR: PH0863; PH0863.  
 DR HSSP: P01607; 1BMW.  
 DR SMR: Q9UL70; 1-108.  
 DR InterPro: IPR003599; Ig.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig v
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
SQ
Query Match 77.3%; Score 420; DB 2; Length 108;
Best Local Similarity 79.2%; Pred. No. 5e-37;
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTYTCRASQRIINTYLNWYQKRGKAPKLLIYAASLQSGVPSRF 60
DB 3 QMTQSPSLASVGDRTYTCRASQGISNLYAWYQKRGKAPKLLIYAASLQSGVPSRF 62
QY 61 SGSGYGTDFLTLLTSLQFEDPASYCOESLSASYTFQGTKEIKR 106
DB 63 SGSGYGTDFLTLLTSLQFEDPASYCOEKNASAPRTFGTKLEIKR 108

RESULT 14
072473_HUMAN PRELIMINARY; PRT; 234 AA.
AC 072473;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE IGKC protein.
GN Name=IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
TX TISSUE=Lung;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Muliyil S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
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CC EMBL; BC056256; AAHS6256.1; -, mRNA.
DR HSSP; P01834; 1HEZ.

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DR SMR; Q72473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; IgC1; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

QY 2 LTQSPSLASVGDRTYTCRASQRIINTYLNWYQKRGKAPKLLIYAASLQSGVPSRF 61
DB 24 MTQSPSLASVGDRTYTCRASQGISNLYAWYQKRGKAPKLLIYAASLQSGVPSRF 63
QY 62 SGSGYGTDFLTLLTSLQFEDPASYCOESLSASYTFQGTKEIKR 106
DB 84 GSASGTDFTLLTSLQFEDPASYCOEYTYTPWTFGTKLEIKR 128

RESULT 15
072473_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RX MEDLINE=71064027; PubMed=4923144;
TX TISSUE=Lung;
RP PROTEIN SEQUENCE.
RA Gotlib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC PIR; A90562; KIHUEU.
DR HSSP; P01607; 1BMW.
DR SMR; P01598; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR013106; V-set.

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DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
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 FT REGION 24 34 /FtId=PRO\_0000059742.  
 FT REGION 35 49 Framework-1.  
 FT REGION 50 56 Complementarity-determining-1.  
 FT REGION 57 88 Framework-2.  
 FT REGION 89 97 Complementarity-determining-2.  
 FT REGION 98 107 Framework-3.  
 FT DISUPID 23 Complementarity-determining-3.  
 FT NON\_TER 23 Framework-4.  
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 76.6%; Score 416; DB 1; Length 108;  
 Best Local Similarity 77.1%; Pred. No. 1.3e-36;  
 Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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 Db 3 QMTQSPSTLSASYGDRVTITCRASQSIINTWLMWYQKPGKAPKLLIMYKASSLSQGVPSRF 62  
 QY 61 SSGSGYGTDFLTITSSLOFEDPFASYCQESLSASYTFGGGTRVEIK 105  
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 Db 63 IGSQSGTEFTLTITSSLOPDDPFATYYCQQYNDSKMFQGGTRVEIK 107  
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Search completed: August 30, 2006, 00:35:16  
 Job time : 58.8182 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 14.4545 Seconds  
(without alignments)  
641.891 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543  
Sequence: 1 ERTQSPSSIASVGDVETIS.....QESLSASYFGQGTKEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued Patents JA:\*  
1: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/ECTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ProdData/2/1aa/Backfill1es1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	87.5	107	1 US-08-276-852-104	Sequence 104, App
2	475	87.5	107	1 US-08-899-575-104	Sequence 104, App
3	475	87.5	107	1 US-08-899-575-104	Sequence 104, App
4	475	87.5	107	5 PCT-US95-08743-104	Sequence 104, App
5	474	87.3	107	2 US-09-240-274-179	Sequence 179, App
6	474	87.3	107	2 US-09-848-798-179	Sequence 179, App
7	472	86.9	107	2 US-09-240-274-33	Sequence 33, App1
8	472	86.9	107	2 US-09-240-274-175	Sequence 175, App
9	472	86.9	107	2 US-09-240-274-176	Sequence 176, App
10	472	86.9	107	2 US-09-848-798-33	Sequence 33, App1
11	472	86.9	107	2 US-09-848-798-175	Sequence 175, App
12	472	86.9	107	2 US-09-848-798-176	Sequence 176, App
13	471	86.7	107	2 US-09-240-274-156	Sequence 156, App
14	471	86.7	107	2 US-09-848-798-156	Sequence 156, App
15	468	86.2	107	2 US-09-240-274-36	Sequence 36, App1
16	468	86.2	107	2 US-09-848-798-36	Sequence 36, App1
17	467	86.0	107	1 US-08-276-852-105	Sequence 105, App
18	467	86.0	107	1 US-08-899-575-105	Sequence 105, App
19	467	86.0	107	1 US-08-899-575-105	Sequence 105, App
20	467	86.0	107	5 PCT-US95-08743-105	Sequence 105, App
21	464.5	85.5	108	2 US-09-240-274-32	Sequence 32, App1
22	464.5	85.5	108	2 US-09-240-274-43	Sequence 43, App1
23	464.5	85.5	108	2 US-09-848-798-32	Sequence 32, App1
24	464.5	85.5	108	2 US-09-848-798-43	Sequence 43, App1
25	464	85.5	107	2 US-09-240-274-37	Sequence 37, App1
26	464	85.5	107	2 US-09-848-798-37	Sequence 37, App1

27	464	85.5	240	2 US-09-192-854-2	Sequence 2, App1
28	464	85.5	240	2 US-09-511-939-2	Sequence 2, App1
29	462	85.1	107	2 US-09-240-274-38	Sequence 38, App1
30	462	85.1	107	2 US-09-240-274-39	Sequence 39, App1
31	462	85.1	107	2 US-09-848-798-38	Sequence 38, App1
32	462	85.1	107	2 US-09-848-798-39	Sequence 39, App1
33	461	84.9	107	2 US-09-240-274-158	Sequence 158, App
34	461	84.9	107	2 US-09-848-798-158	Sequence 158, App
35	460.5	84.8	108	2 US-09-240-274-167	Sequence 167, App
36	460.5	84.8	108	2 US-09-848-798-167	Sequence 167, App
37	459.5	84.6	108	2 US-09-240-274-163	Sequence 163, App
38	459.5	84.6	108	2 US-09-848-798-163	Sequence 163, App
39	458	84.3	107	2 US-09-240-274-35	Sequence 35, App1
40	458	84.3	107	2 US-09-240-274-173	Sequence 173, App
41	458	84.3	107	2 US-09-240-274-173	Sequence 173, App
42	458	84.3	107	2 US-09-848-798-35	Sequence 35, App1
43	458	84.3	108	2 US-09-848-798-173	Sequence 173, App
44	457	84.2	104	1 US-08-379-057-29	Sequence 29, App1
45	457	84.2	104	1 US-08-276-852-106	Sequence 106, App

#### ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbae, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OR INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.4e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDFLTITSSLOPEDFASYYCOESLSASTTFCGKTVEIKR 106  
DB 61 SSGSGTDFLTITSSLOPEDFATYYCOOSYSTPYTFQGTKEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.4e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDFLTITSSLOPEDFASYYCOESLSASTTFCGKTVEIKR 106  
DB 61 SSGSGTDFLTITSSLOPEDFATYYCOOSYSTPYTFQGTKEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCR1452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.4e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDFLTITSSLOPEDFASYYCOESLSASTTFCGKTVEIKR 106  
DB 61 SSGSGTDFLTITSSLOPEDFATYYCOOSYSTPYTFQGTKEIKR 106

RESULT 4  
PCT-US95-08743-104

; Sequence 104, Application PC/TUS9508743  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; NUMBER OF SEQUENCES: 170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION NUMBER:  
; FILING DATE: 11-JUL-1995  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-08743-104

Query Match 87.5%; Score 475; DB 5; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.4e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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Db 1 ELTQSPSSLSASVGDVVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 60  
Qy 61 SSGSGYTDFTLTITSSLOQPEDFASYCQESLSASYTFGQGTKEIKR 106  
Db 61 SSGSGYTDFTLTITSSLOQPEDFATYTCQSYSTPTFGQGTKEIKR 106

## RESULT 5

US-09-240-274-179  
; Sequence 179, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 179  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-240-274-179

Query Match 87.3%; Score 474; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.8e-38;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYOHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 61  
Qy 61 SSGSGYTDFTLTITSSLOQPEDFASYCQESLSASYTFGQGTKEIKR 106  
Db 61 SSGSGYTDFTLTITSSLOQPEDFATYTCQSYSTPTFGQGTKEIKR 106

Db 62 SSGSGYTDFTLTITSSLOQPEDFATYTCQSYSTPTFGQGTKEIKR 107

## RESULT 6

US-09-848-798-179  
; Sequence 179, Application US/09848798  
; Patent No. 6858719  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; EARLIER FILING DATE: 2001-05-04  
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 179  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-179

Query Match 87.3%; Score 474; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.8e-38;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYOHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 61  
Qy 61 SSGSGYTDFTLTITSSLOQPEDFASYCQESLSASYTFGQGTKEIKR 106  
Db 62 SSGSGYTDFTLTITSSLOQPEDFATYTCQSYSTPTFGQGTKEIKR 107

## RESULT 7

US-09-240-274-33  
; Sequence 33, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; EARLIER FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-240-274-33

Query Match 86.9%; Score 472; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 2.8e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLNWYOHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOQSYSTLMTFGQGTVEIKR 107

## RESULT 8

US-09-240-274-175  
; Sequence 175, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 175  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-240-274-175

Query Match 86.9%; Score 472; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.8e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITSCRASORINTYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTOSPSLSASVGDRTVITSCRASQSISSYLMWYQKPKAPKLLIYAASSLSQGVPSRF 61  
Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOQSYSTLMTFGQGTVEIKR 107

## RESULT 9

US-09-240-274-176  
; Sequence 176, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 176  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-240-274-176

Query Match 86.9%; Score 472; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.8e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITSCRASORINTYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTOSPSLSASVGDRTVITSCRASQSISSYLMWYQKPKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOQSYSTLMTFGQGTVEIKR 107

## RESULT 10

US-09-848-798-33  
; Sequence 33, Application US/09848798  
; Patent No. 6858719  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-848-798-33

Query Match 86.9%; Score 472; DB 2; Length 107;  
Best Local Similarity 87.7%; Pred. No. 2.8e-38;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGDRTVITSCRASORINTYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTOSPSLSASVGDRTVITSCRASQSISSYLMWYQKPKAPKLLIYAASSLSQGVPSRF 61  
Qy 61 SSGSGYDFTLTITSSLOPEDFASYYCOESLSASTYFGQGTVEIKR 106  
Db 62 SSGSGYDFTLTITSSLOPEDFATYYCOQSYSTLMTFGQGTVEIKR 107

## RESULT 11

US-09-848-798-175  
; Sequence 175, Application US/09848798  
; Patent No. 6858719  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 175  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-09-848-798-175

Query Match 86.9%; Score 472; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.8e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Best Local Similarity 86.8%; Pred. No. 2.8e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVITITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVTFGQGTKEIKR 106  
Db 62 SSGSGGTDFLTITSSLOPEDFATVYCOQSYSTPTFTGQGTKEIKR 107

## RESULT 12

US-09-848-798-176  
; Sequence 176, Application US/09848798

; Patent No. 6858719  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/028,550  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 176  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
; US-09-848-798-176

Query Match 86.9%; Score 472; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 2.8e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVITITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVTFGQGTKEIKR 106  
Db 62 SSGSGGTDFLTITSSLOPEDFATVYCOQSYSTPTFTGQGTKEIKR 107

## RESULT 13

US-09-240-274-156  
; Sequence 156, Application US/09240274

; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 156  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13

## US-09-240-274-156

Query Match 86.7%; Score 471; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 3.5e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVITITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVTFGQGTKEIKR 106  
Db 62 SSGSGGTDFLTITSSLOPEDFATVYCOQSYSTPTFTGQGTKEIKR 107

## RESULT 14

US-09-848-798-156  
; Sequence 156, Application US/09848798

; Patent No. 6858719  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT FILING DATE: 2001-05-04  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/028,550  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 156  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
; US-09-848-798-156

Query Match 86.7%; Score 471; DB 2; Length 107;  
Best Local Similarity 86.8%; Pred. No. 3.5e-38;  
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASORINTYLMNYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
Db 2 ELTQSPSSLSASVGDVITITCRASQSISSYLMNYQOKPGKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASVYCOESLSASVTFGQGTKEIKR 106  
Db 62 SSGSGGTDFLTITSSLOPEDFATVYCOQSYSTPTFTGQGTKEIKR 107

## RESULT 15

US-09-240-274-36  
; Sequence 36, Application US/09240274

; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 107  
; TYPE: PRT



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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 60.7091 Seconds  
(without alignments)  
808.788 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGRVTS.....QESLSASYFGQGTKEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/Ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/Ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/Ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/Ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/Ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/Ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	106	4	US-10-027-725A-10 Sequence 10, Appl1
2	475	87.5	107	4	US-10-016-986-104 Sequence 104, App
3	474	87.3	107	3	US-09-848-798-179 Sequence 179, App
4	474	87.3	107	6	US-11-064-174-179 Sequence 179, App
5	472	86.9	107	3	US-09-848-798-175 Sequence 33, Appl1
6	472	86.9	107	3	US-09-848-798-175 Sequence 175, App
7	472	86.9	107	3	US-09-848-798-176 Sequence 176, App
8	472	86.9	107	6	US-11-064-174-175 Sequence 33, Appl1
9	472	86.9	107	6	US-11-064-174-175 Sequence 175, App
10	472	86.9	107	6	US-11-064-174-175 Sequence 175, App
11	471	86.7	107	3	US-09-848-798-156 Sequence 156, App
12	471	86.7	107	6	US-11-064-174-156 Sequence 156, App
13	468	86.2	107	3	US-09-848-798-36 Sequence 36, Appl1
14	468	86.2	107	6	US-11-064-174-36 Sequence 36, Appl1
15	468	86.2	116	5	US-10-783-311-198 Sequence 198, App
16	467	86.0	107	4	US-10-016-986-105 Sequence 105, App
17	465	85.6	111	4	US-10-203-754A-57 Sequence 57, Appl1
18	464.5	85.5	108	3	US-09-848-798-32 Sequence 32, Appl1
19	464.5	85.5	108	3	US-09-848-798-43 Sequence 43, Appl1
20	464.5	85.5	108	6	US-11-064-174-32 Sequence 32, Appl1
21	464.5	85.5	108	6	US-11-064-174-43 Sequence 43, Appl1
22	464	85.5	107	6	US-09-848-798-37 Sequence 37, Appl1
23	464	85.5	107	6	US-11-064-174-37 Sequence 37, Appl1
24	464	85.5	108	4	US-10-409-814A-4 Sequence 4, Appl1
25	464	85.5	108	5	US-10-925-366A-3 Sequence 3, Appl1
26	464	85.5	108	5	US-10-925-366A-6 Sequence 6, Appl1
27	464	85.5	108	6	US-11-102-512-3 Sequence 3, Appl1

28	464	85.5	108	6	US-11-102-512-6 Sequence 6, Appl1
29	464	85.5	108	6	US-11-098-758-3 Sequence 3, Appl1
30	464	85.5	108	6	US-11-098-758-6 Sequence 6, Appl1
31	464	85.5	108	6	US-11-166-496-10 Sequence 10, Appl1
32	464	85.5	240	3	US-09-192-854-2 Sequence 2, Appl1
33	464	85.5	240	3	US-09-968-561A-2 Sequence 2, Appl1
34	464	85.5	240	3	US-09-968-744A-2 Sequence 2, Appl1
35	464	85.5	240	3	US-09-968-561A-2 Sequence 2, Appl1
36	464	85.5	240	5	US-10-744-774-1 Sequence 1, Appl1
37	464	85.5	240	5	US-10-925-366A-219 Sequence 219, App
38	464	85.5	240	6	US-11-115-682-2 Sequence 2, Appl1
39	464	85.5	240	6	US-11-098-758-219 Sequence 219, App
40	463	85.3	107	3	US-09-791-153A-67 Sequence 67, Appl1
41	463	85.3	108	5	US-10-726-332-214 Sequence 214, App
42	463	85.3	108	5	US-10-805-177-64 Sequence 64, Appl1
43	462	85.1	106	4	US-10-027-725A-12 Sequence 12, Appl1
44	462	85.1	107	3	US-09-848-798-38 Sequence 38, Appl1
45	462	85.1	107	3	US-09-848-798-39 Sequence 39, Appl1

#### ALIGNMENTS

```
RESULT 1
US-10-027-725A-10
; Sequence 10, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Pickner, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-10

Query Match      100.0%; Score 543; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ELTQSPSSLSASVGRVTSICRASQRIINTYLMWYQHKPKAPKLLIYAASSLQSGVPSRF 60
      |||
DB      1  ELTQSPSSLSASVGRVTSICRASQRIINTYLMWYQHKPKAPKLLIYAASSLQSGVPSRF 60
QY      61  SSGSYGTDTLTITSSIQEFDPASYQESLSASYTGQGTKEIKR 106
      |||
DB      61  SSGSYGTDTLTITSSIQEFDPASYQESLSASYTGQGTKEIKR 106

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/999,575
; PRIOR FILING DATE: 1997-07-24
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PRIOR APPLICATION NUMBER: US 08/276,852  
PRIOR FILING DATE: 1994-07-18  
PRIOR APPLICATION NUMBER: US 08/178,302  
PRIOR FILING DATE: 1994-01-06  
PRIOR APPLICATION NUMBER: PCT/US93/09328  
PRIOR FILING DATE: 1993-09-30  
PRIOR APPLICATION NUMBER: US 07/954,148  
PRIOR FILING DATE: 1992-09-30  
NUMBER OF SEQ ID NOS: 176  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 104  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized  
US-10-016-986-104

Query Match 87.5%; Score 475; DB 4; Length 107;  
Best Local Similarity 87.7%; Pred. No. 6,9e-36;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDVDTITCRASQSISSYLMYQOKPKAPKLLIYAASSLSQGVPSRF 60  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTPGQGTKEIKR 106  
DB 61 SSGSGGTDFLTITSSLOPEDFATYCCQOSYSTPTWTFGQGTKEIKR 106

## RESULT 3

US-09-848-798-179  
Sequence 179, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 179  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-179

Query Match 87.3%; Score 474; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 8.5e-36;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSMSASVGDVDTITCRASQSICTITLMYQOKPKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTPGQGTKEIKR 106  
DB 62 SSGSGGTDFLTITSSLOPEDFATYCCQOSYSTPTWTFGQGTKEIKR 107

RESULT 4  
US-11-064-174-179  
Sequence 179, Application US/11064174  
Publication No. US20050282252A1

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/11/064,174  
CURRENT FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 179  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-11-064-174-179

Query Match 87.3%; Score 474; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 8.5e-36;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSMSASVGDVDTITCRASQSICTITLMYQOKPKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTPGQGTKEIKR 106  
DB 62 SSGSGGTDFLTITSSLOPEDFATYCCQOSYSTPTWTFGQGTKEIKR 107

## RESULT 5

US-09-848-798-33  
Sequence 33, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 33  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-848-798-33

Query Match 86.3%; Score 472; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.3e-35;  
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVDTISCRASQRIINTYLMYQHKPKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVDTITCRASQSISSYLMYQOKPKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTPGQGTKEIKR 106  
DB 62 SSGSGGTDFLTITSSLOPEDFATYCCQOSYSTPTWTFGQGTKEIKR 107



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RESULT 6
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYDTFTLTITSSLPEDFASYCOQSYSTPWTGQGTKEIKR 106
DB 62 SSGSGYDTFTLTITSSLPEDFATYCCQSYSTPWTGQGTKEIKR 107

RESULT 7
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYDTFTLTITSSLPEDFASYCOQSYSTPWTGQGTKEIKR 106
DB 62 SSGSGYDTFTLTITSSLPEDFATYCCQSYSTPWTGQGTKEIKR 107
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DB 62 SSGSGYDTFTLTITSSLPEDFATYCCQSYSTPWTGQGTKEIKR 107

RESULT 8
US-11-064-174-33
; Sequence 33, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-11-064-174-33

Query Match      86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTISCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYDTFTLTITSSLPEDFASYCOQSYSTPWTGQGTKEIKR 106
DB 62 SSGSGYDTFTLTITSSLPEDFATYCCQSYSTPWTGQGTKEIKR 107

RESULT 9
US-11-064-174-175
; Sequence 175, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-064-174-175

Query Match      86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
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Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTPTWTFGGTKVEIKR 107

RESULT 10
US-11-064-174-176
; Sequence 176, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-064-174-176

Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTPTWTFGGTKVEIKR 107

RESULT 11
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match 86.7%; Score 471; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTPTWTFGGTKVEIKR 107

RESULT 12
US-11-064-174-156
; Sequence 156, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-064-174-156

Query Match 86.7%; Score 471; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRF 61
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTPTWTFGGTKVEIKR 107

RESULT 13
US-09-848-798-36
; Sequence 36, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 36  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I05  
US-09-848-798-36

Query Match 86.2%; Score 468; DB 3; Length 107;  
Best Local Similarity 86.8%; Pred. No. 3e-35;  
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYTDFTLTITSSLOPEDFASYCOESLSASYTFGGQTKVEIKR 106  
DB 62 TSGSGCTDFTLTITSSLOPEDFATYCCQSYSTRMTGQGTKEIKR 107

## RESULT 14

US-11-064-174-36  
Sequence 36, Application US/11064174  
Publication No. US2005028252A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/11/064,174  
CURRENT FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I05  
US-11-064-174-36

Query Match 86.2%; Score 468; DB 6; Length 107;  
Best Local Similarity 86.8%; Pred. No. 3e-35;  
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 61  
QY 61 SSGSGYTDFTLTITSSLOPEDFASYCOESLSASYTFGGQTKVEIKR 106  
DB 62 TSGSGCTDFTLTITSSLOPEDFATYCCQSYSTRMTGQGTKEIKR 107

## RESULT 15

US-10-783-311-198  
Sequence 198, Application US/10783311  
Publication No. US2005009136A1  
GENERAL INFORMATION:  
APPLICANT: Nixon, Andrew  
TITLE OF INVENTION: PAPP-A LIGANDS  
FILE REFERENCE: 10280-059001  
CURRENT APPLICATION NUMBER: US/10/783,311  
CURRENT FILING DATE: 2004-02-19  
PRIOR APPLICATION NUMBER: US 60/448,515

PRIOR FILING DATE: 2003-02-19  
NUMBER OF SEQ ID NOS: 394  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 198  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Light Chain amino acid sequence  
US-10-783-311-198

Query Match 86.2%; Score 468; DB 5; Length 116;  
Best Local Similarity 85.8%; Pred. No. 3.3e-35;  
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60  
DB 4 QMTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQHPKAPKLLIYAASSLSQGVPSRF 63  
QY 61 SSGSGYTDFTLTITSSLOPEDFASYCOESLSASYTFGGQTKVEIKR 106  
DB 64 SSGSGCTDFTLTITSSLOPEDFATYCCQSYSTRMTGQGTKEIKR 109

Search completed: August 30, 2006, 00:50:40  
Job time : 61.7091 secs

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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 12.5273 Seconds  
(without alignments)  
578.960 Million cell updates/sec

Title: US-10-027-725a-10

Perfect score: 543  
Sequence: 1 ELTQSPSSLSASVGDVTVIS.....QESLSASYFGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/FCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ProdData/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474	87.3	107	7	US-11-328-483-179 Sequence 179, App
2	472	86.9	107	7	US-11-328-483-33 Sequence 33, App1
3	472	86.9	107	7	US-11-328-483-175 Sequence 175, App
4	472	86.9	107	7	US-11-328-483-176 Sequence 176, App
5	471	86.7	107	7	US-11-328-483-156 Sequence 156, App1
6	468	86.2	106	7	US-11-337-300-41 Sequence 41, App1
7	468	86.2	107	7	US-11-328-483-36 Sequence 36, App1
8	468	86.2	243	7	US-11-337-300-47 Sequence 47, App1
9	468	86.2	244	7	US-11-317-786B-17 Sequence 17, App1
10	468	86.2	244	7	US-11-317-786B-19 Sequence 19, App1
11	468	86.2	245	7	US-11-337-300-51 Sequence 51, App1
12	468	86.2	245	7	US-11-337-300-53 Sequence 53, App1
13	468	86.2	245	7	US-11-337-300-59 Sequence 59, App1
14	468	86.2	245	7	US-11-337-300-63 Sequence 63, App1
15	468	86.2	247	7	US-11-337-300-57 Sequence 57, App1
16	468	86.2	247	7	US-11-337-300-96 Sequence 96, App1
17	468	86.2	248	7	US-11-337-300-61 Sequence 61, App1
18	468	86.2	249	7	US-11-337-300-49 Sequence 49, App1
19	468	86.2	249	7	US-11-337-300-67 Sequence 67, App1
20	468	86.2	249	7	US-11-337-300-69 Sequence 69, App1
21	468	86.2	249	7	US-11-337-300-92 Sequence 90, App1
22	468	86.2	249	7	US-11-337-300-90 Sequence 92, App1
23	464.5	85.5	108	7	US-11-328-483-32 Sequence 32, App1
24	464.5	85.5	108	7	US-11-328-483-43 Sequence 43, App1
25	464	85.5	107	7	US-11-328-483-37 Sequence 37, App1

26	463	85.3	214	7	US-11-337-300-129 Sequence 129, App
27	463	85.3	214	7	US-11-317-786B-13 Sequence 13, App1
28	463	85.3	245	6	US-10-539-402-16 Sequence 16, App1
29	462	85.1	107	7	US-11-328-483-38 Sequence 38, App1
30	462	85.1	107	7	US-11-328-483-39 Sequence 39, App1
31	461	84.9	107	7	US-11-328-483-158 Sequence 158, App
32	460.5	84.8	108	7	US-11-328-483-167 Sequence 167, App
33	459.5	84.6	108	7	US-11-328-483-163 Sequence 163, App
34	459	84.5	109	7	US-11-328-483-163 Sequence 9, App1
35	458	84.3	107	7	US-11-328-483-35 Sequence 35, App1
36	458	84.3	107	7	US-11-328-483-173 Sequence 173, App
37	457	84.2	107	7	US-11-328-483-40 Sequence 40, App1
38	457	84.2	240	7	US-11-317-786B-15 Sequence 15, App1
39	456	84.0	107	7	US-11-328-483-44 Sequence 44, App1
40	455	83.8	107	7	US-11-328-483-103 Sequence 103, App
41	454	83.6	109	7	US-11-375-221-103 Sequence 39, App1
42	454	83.6	109	7	US-11-094-132-75 Sequence 75, App1
43	453	83.4	105	7	US-11-333-197-52 Sequence 52, App1
44	452	83.2	107	7	US-11-328-483-172 Sequence 172, App
45	452	83.2	107	7	US-11-328-483-174 Sequence 174, App
			291	7	US-11-154-103-10 Sequence 10, App1

## ALIGNMENTS

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RESULT 1
US-11-328-483-179
; Sequence 179, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: (Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-328-483-179

Query Match      87.3%; Score 474; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.5e-37;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDVTVISCRASQRIINTYLMWYQKPGKAPLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSMSASVGDVTVITCRASQSIGTYLMWYQKPGKAPLLIYAASSLSQGVPSRF 61
Cy 61 SSGSGVDTFTLTSSLOPEDPASVYQESLSASYTFGQGTKEIKR 106
Db 62 SSGSGDTFTLTSSLOPEDFATVYQOSYSTPMTFGQGTKEIKR 107

RESULT 2
US-11-328-483-33
; Sequence 33, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
```

```

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-11-328-483-33

```

```

Query Match          86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 3,8e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 ELTOSPSLSASVGDRTYISCRASORINTYINWYQHKPGKAPKLLIYAASLSQGVPSRF 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2 ELTOSPSLSASVGDRTYITCRASOSISSTYINWYQKPGKAPKLLIYAASLSQGVPSRF 61
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      61 SSGSGYGTDFLTITSLQPEDFASYYCOESLSASYTFGGGTKEIKR 106
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      62 SSGSGGTDFLTITSLQPEDFATYYCOQSYSTPMTFGGTKEIKR 107
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 3
US-11-328-483-175
; Sequence 175, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-328-483-175

```

```

Query Match          86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 3,8e-37;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 ELTOSPSLSASVGDRTYISCRASORINTYINWYQHKPGKAPKLLIYAASLSQGVPSRF 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2 ELTOSPSLSASVGDRTYITCRASOSISSTYINWYQKPGKAPKLLIYAASLSQGVPSRF 61
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY      61 SSGSGYGTDFLTITSLQPEDFASYYCOESLSASYTFGGGTKEIKR 106
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      62 SSGSGGTDFLTITSLQPEDFATYYCOQSYSTPMTFGGTKEIKR 107
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 4
US-11-328-483-176
; Sequence 176, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-328-483-176

```

```

Query Match          86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 3,8e-37;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

```

```

QY      1 ELTOSPSLSASVGDRTYISCRASORINTYINWYQHKPGKAPKLLIYAASLSQGVPSRF 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2 ELTOSPSLSASVGDRTYITCRASOSISSTYINWYQKPGKAPKLLIYAASLSQGVPSRF 61
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      61 SSGSGYGTDFLTITSLQPEDFASYYCOESLSASYTFGGGTKEIKR 106
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      62 SSGSGGTDFLTITSLQPEDFATYYCOQSYSTPMTFGGTKEIKR 107
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 5
US-11-328-483-156
; Sequence 156, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```



;; CURRENT FILING DATE: 2005-12-22  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 17  
;; LENGTH: 244  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Amino acid sequence of SC02-378, synthetic  
US-11-317-786B-17

Query Match 86.2%; Score 468; DB 7; Length 244;  
Best Local Similarity 87.7%; Pred. No. 2e-36;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 136 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 195  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGCGTKVEIKR 106  
DB 196 SSGSGGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 241

RESULT 10  
US-11-317-786B-19

;; Sequence 19, Application US/11317786B  
;; Publication No. US2006017451A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Van den Oudenrijn, Sonja  
;; APPLICANT: Bakker, Alexander B.H.  
;; APPLICANT: Bakker, Adrianus O.  
;; APPLICANT: Van Melijer, Marja  
;; TITLE OF INVENTION: BINDING MOLECULES FOR THE TREATMENT OF MTELOID CELL MALIGNANCIES  
;; FILE REFERENCE: 0090 WO 00 ORD 2578-7546US  
;; CURRENT FILING DATE: 2005-12-22  
;; CURRENT APPLICATION NUMBER: US/11/317,786B  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 19  
;; LENGTH: 244  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: Amino acid sequence of SC02-161, synthetic  
US-11-317-786B-19

Query Match 86.2%; Score 468; DB 7; Length 244;  
Best Local Similarity 87.7%; Pred. No. 2e-36;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 136 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 195  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGCGTKVEIKR 106  
DB 196 SSGSGGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 241

RESULT 11  
US-11-337-300-51

;; Sequence 51, Application US/11337300  
;; Publication No. US20060121580A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Crucell Holland B.V.  
;; APPLICANT: ter Meulen, Jan H.  
;; APPLICANT: De Kruijf, Cornelis A.  
;; APPLICANT: van den Brink, Edward N.  
;; APPLICANT: Goudsmilt, Jaap  
;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
;; FILE REFERENCE: 0091 WO 00 ORD  
;; CURRENT APPLICATION NUMBER: US/11/337,300

;; CURRENT FILING DATE: 2006-01-20  
;; NUMBER OF SEQ ID NOS: 478  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 51  
;; LENGTH: 245  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: SC03-003  
US-11-337-300-51

Query Match 86.2%; Score 468; DB 7; Length 245;  
Best Local Similarity 87.7%; Pred. No. 2e-36;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 137 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 196  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGCGTKVEIKR 106  
DB 197 SSGSGGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 242

RESULT 12  
US-11-337-300-53

;; Sequence 53, Application US/11337300  
;; Publication No. US20060121580A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Crucell Holland B.V.  
;; APPLICANT: ter Meulen, Jan H.  
;; APPLICANT: De Kruijf, Cornelis A.  
;; APPLICANT: van den Brink, Edward N.  
;; APPLICANT: Goudsmilt, Jaap  
;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
;; FILE REFERENCE: 0091 WO 00 ORD  
;; CURRENT FILING DATE: 2006-01-20  
;; CURRENT APPLICATION NUMBER: US/11/337,300  
;; NUMBER OF SEQ ID NOS: 478  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 53  
;; LENGTH: 245  
;; TYPE: PRT  
;; ORGANISM: Artificial sequence  
;; FEATURE:  
;; OTHER INFORMATION: SC03-005  
US-11-337-300-53

Query Match 86.2%; Score 468; DB 7; Length 245;  
Best Local Similarity 87.7%; Pred. No. 2e-36;  
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60  
DB 137 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 196  
QY 61 SSGSGYGTDFLTITSSLOPEDFASYYCOESLSASVTFGCGTKVEIKR 106  
DB 197 SSGSGGTDFLTITSSLOPEDFATYYCOQSYSTPPTFGCGTKVEIKR 242

RESULT 13  
US-11-337-300-59

;; Sequence 59, Application US/11337300  
;; Publication No. US20060121580A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Crucell Holland B.V.  
;; APPLICANT: ter Meulen, Jan H.  
;; APPLICANT: De Kruijf, Cornelis A.  
;; APPLICANT: van den Brink, Edward N.  
;; APPLICANT: Goudsmilt, Jaap  
;; TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
;; FILE REFERENCE: 0091 WO 00 ORD



```
/ CURRENT APPLICATION NUMBER: US/11/337,300
/ CURRENT FILING DATE: 2006-01-20
/ NUMBER OF SEQ ID NOS: 478
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 59
/ LENGTH: 245
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: SC03-008
US-11-337-300-59
```

```
Query Match      86.2%; Score 468; DB 7; Length 245;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 137 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 196
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGGGTKEIKR 106
DB 197 SSGSGYGTDFLTITSSLOPEDFATYYCOOSYSTPTPTFGGTKEIKR 242
```

## RESULT 14

```
US-11-337-300-63
/ Sequence 63, Application US/11337300
/ Publication No. US20060121580A1
/ GENERAL INFORMATION:
/ APPLICANT: Crucell Holland B.V.
/ APPLICANT: ter Meulen, Jan H.
/ APPLICANT: De Kruif, Cornelis A.
/ APPLICANT: van den Brink, Edward N.
/ APPLICANT: Goudamit, Jaap
/ TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
/ FILE REFERENCE: 0091 WO 00 ORD
/ CURRENT APPLICATION NUMBER: US/11/337,300
/ CURRENT FILING DATE: 2006-01-20
/ NUMBER OF SEQ ID NOS: 478
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 63
/ LENGTH: 245
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: SC03-010
US-11-337-300-63
```

```
Query Match      86.2%; Score 468; DB 7; Length 245;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 137 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 196
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGGGTKEIKR 106
DB 197 SSGSGYGTDFLTITSSLOPEDFATYYCOOSYSTPTPTFGGTKEIKR 242
```

## RESULT 15

```
US-11-337-300-57
/ Sequence 57, Application US/11337300
/ Publication No. US20060121580A1
/ GENERAL INFORMATION:
/ APPLICANT: Crucell Holland B.V.
/ APPLICANT: ter Meulen, Jan H.
/ APPLICANT: De Kruif, Cornelis A.
/ APPLICANT: van den Brink, Edward N.
/ APPLICANT: Goudamit, Jaap
/ TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof
```

```
/ FILE REFERENCE: 0091 WO 00 ORD
/ CURRENT APPLICATION NUMBER: US/11/337,300
/ CURRENT FILING DATE: 2006-01-20
/ NUMBER OF SEQ ID NOS: 478
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 57
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: SC03-007
US-11-337-300-57
```

```
Query Match      86.2%; Score 468; DB 7; Length 247;
Best Local Similarity 87.7%; Pred. No. 2.1e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLMWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 139 ELTQSPSSLSASVGDRTVITCRASQSISSYLMWYQKPGKAPKLLIYAASSLSQGVPSRF 198
QY 61 SSGSGYGTDFLTITSSLOPEDFASYCOESLSASYTFGGGTKEIKR 106
DB 199 SSGSGYGTDFLTITSSLOPEDFATYYCOOSYSTPTPTFGGTKEIKR 244
```

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Search completed: August 30, 2006, 00:52:03
Job time : 12.5273 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 95.2394 Seconds  
(without alignments)  
508.875 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547  
Sequence: 1 ELVQSPSSIASVGDVRVIT.....QOSYTTLYTFSGSKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq.8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	537	98.2	106	5 ABG30449
2	486	88.8	115	10 AEG01347
3	484	88.5	107	2 AAW01283
4	484	88.5	107	2 AAW01283
5	484	88.5	107	3 AAY95135
6	484	88.5	107	3 AAY95135
7	483	88.3	107	4 AAG33590
8	483	88.3	107	4 ABO27397
9	480	87.8	107	6 AAG33644
10	480	87.8	107	6 ABO27451
11	480	87.8	107	6 ABO27451
12	478	87.4	115	10 AEG01281
13	476	87.0	107	2 AAW01284
14	476	87.0	107	3 AAY95136
15	476	87.0	107	3 AAY95136
16	476	87.0	107	3 AAY95136
17	476	87.0	107	3 AAY95136
18	475	86.8	107	4 AAG33663
19	475	86.8	107	4 AAG33664
20	475	86.8	107	6 ABO27471
21	475	86.8	107	6 ABO27470
22	475	86.8	107	10 ABE74547
23	475	86.8	107	10 ABE74548

24	474	86.7	107	4 AAG33667	Aag33667 Human ant
25	474	86.7	107	6 ABO27474	Abc27474 Anti-Rh(D
26	474	86.7	107	10 ABE74653	Aee74653 Anti-Rh(D
27	474	86.7	107	10 ABE74551	Aee74551 Anti-Rh(D
28	474	86.7	214	10 AEF65392	Aef65392 Anti-RhD
29	473.5	86.6	108	4 AAG33589	Aag33589 Human ant
30	473.5	86.6	108	4 AAG33600	Aag33600 Human ant
31	473.5	86.6	108	6 ABO27407	Abc27407 Anti-Rh(D
32	473.5	86.6	108	6 ABO27396	Abc27396 Anti-Rh(D
33	473.5	86.6	108	6 ABE74415	Aee74415 Anti-Rh(D
34	473.5	86.6	108	10 ABE74404	Aee74404 Anti-Rh(D
35	473	86.5	107	4 AAG33594	Aag33594 Human ant
36	473	86.5	107	6 ABO27401	Abc27401 Anti-Rh(D
37	473	86.5	107	10 ABE74409	Aee74409 Anti-Rh(D
38	473	86.5	109	8 ADP66620	Adp66620 Anti-RAS
39	473	86.5	109	8 ADP66619	Adp66619 Anti-RAS
40	473	86.5	109	8 ADP66623	Adp66623 Anti-RAS
41	473	86.5	109	8 ADP66624	Adp66624 Anti-RAS
42	473	86.5	109	8 ADO79343	Ado79343 Anti-RAS
43	473	86.5	109	8 ADO79344	Ado79344 Anti-RAS
44	473	86.5	111	4 AAG63656	Aag63656 Amino aci
45	473	86.5	111	6 ABJ38615	Abj38615 Hepatitis

## ALIGNMENTS

RESULT 1	ABG30449	standard; protein; 106 AA.
ID	ABG30449	
XX	ABG30449	
AC	ABG30449	
XX	ABG30449	
DT	21-OCT-2002	(first entry)
XX	Human IGE Fab clone 60 light chain protein.	
XX	Human; fab; anti-allergic; vaccine; grass pollen; Phl p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	Region	1..21
FT	Region	/note="FRL region"
FT	Region	22..32
FT	Region	/note="CDR1 region"
FT	Region	33..47
FT	Region	/note="FR2 region"
FT	Region	48..54
FT	Region	/note="CDR2 protein"
FT	Region	55..86
FT	Region	/note="FR3 region"
FT	Region	87..95
FT	Region	/note="CDR2 region"
FT	Region	96..104
FT	Region	/note="FR4 region"
FT	Misc-difference	98
FT	Misc-difference	/note="Encoded by CCT"
PN	WO200253595-A1	
PD	11-JUL-2002	
XX	27-DEC-2001	2001WO-SE002908.
XX	29-DEC-2000	2000SE-00004892.
XX	(PHAA ) PHARMACIA DIAGNOSTICS AB.	
XX	Flicker S, Steinberger P, Kraft D, Valenta R;	
PI	WPI, 2002-583604/62.	

DR N-PSDB; ABK69641.  
XX  
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
XX Disclosure; Page 40; 45pp; English.  
XX  
XX This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have anti-allergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG  
CC Fab, clone 60 light chain protein of the invention  
XX  
SQ Sequence 106 AA:  
Query Match 98.2%; Score 537, DB 5; Length 106;  
Best Local Similarity 99.1%; Pred. No. 7e-30;  
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDVVTITTCRAPOSISTYLNMYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDVVTITTCRAPOSISTYLNMYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
61 SGSGSGTEFTLTISNLQFEDPASYYCOQSYTTLTYTFGSGTKLEIKR 106  
DB 61 SGSGSGTEFTLTISNLQFEDPASYYCOQSYTTLTYTFGSGTKLEIKR 106  
RESULT 2  
AEG01347 standard; protein; 115 AA.  
XX  
AC AEG01347;  
XX  
DT 20-APR-2006 (first entry)  
XX  
DE Kallikrein 1 antibody light chain variable region SEQ ID NO:1174.  
XX  
KW Antibody, light chain variable region; kallikrein 1; therapeutic;  
KW Antiacetabular; Respiratory-Gen.; Neuroprotective; Antipneumatic;  
KW Antineumatic; Antiallergic; Osteopathic; Antiallergic;  
KW Antineumatic; Gastrointestinal-Gen.; Antidiabetic; Cystostatic;  
KW Cardiovascular-Gen.; uteropathic; Angiogenesis inhibitor; asthma;  
KW Chronic obstructive pulmonary disease; multiple sclerosis; psoriasis;  
KW Rheumatoid arthritis; osteoarthritis; allergic rhinitis; sinusitis;  
KW Inflammatory bowel disease; diabetes; pancreatitis;  
KW Interstitial cystitis; neoplasm; pancreatic ductal adenocarcinoma; tumor;  
KW angiogenesis; cardiovascular disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2006017538-A2.  
XX  
PD 16-FEB-2006.  
XX  
PF 03-AUG-2005; 2005WO-US027493.  
XX  
PR 03-AUG-2004; 2004US-0598506P.  
PR 04-OCT-2004; 2004US-0615721P.  
XX  
PA (DYAX-) DYAX CORP.

XX  
PI Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q;  
XX  
XX WPI, 2006-184027/19.  
DR  
XX  
XX Novel protein comprising immunoglobulin heavy and light chain variable  
PT domain sequences, capable of inhibiting human tissue kallikrein-1  
PT enzymatic activity, useful for treating human tissue kallikrein-1  
PT associated disorder, e.g. asthma.  
XX  
XX Example; SEQ ID NO 1174; 178pp; English.  
XX  
XX The invention relates to a protein (I) comprising an immunoglobulin heavy  
CC chain (HC) variable domain sequence and an immunoglobulin light chain  
CC (LC) variable domain sequence, where the HC variable domain sequence and  
CC the LC variable domain sequence form an antigen binding site binding to  
CC human tissue kallikrein-1 (hkl) and inhibit enzymatic activity of hkl.  
CC Also included is a pharmaceutical composition (II) comprising the protein  
CC and carrier. The protein is useful for treating or preventing an hkl  
CC associated disorder, which involves administering (I) to a subject to  
CC treat or prevent the hkl associated disorder. The disorder is chosen from  
CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,  
CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,  
CC inflammatory bowel diseases, immune mediated diabetes, acute  
CC pancreatitis, interstitial cystitis or neoplastic disorder. The disorder  
CC is asthma and the asthma is allergic or non-allergic asthma. The disorder  
CC is a neoplastic disorder, which is metastatic pancreatic adenocarcinoma  
CC or tumor angiogenesis. The method further involves administering a second  
CC agent that modulates angiogenesis. The second agent is an anti-vascular  
CC endothelial growth factor (VEGF) antibody or its antigen binding  
CC fragment. The protein is useful for modulating an hkl activity, for  
CC detecting the presence of an hkl protein in vitro, for detecting the  
CC presence of an hkl in vivo in a human subject, and for reducing the  
CC angiogenesis associated with cardiovascular disorders. The present  
CC sequence is the light chain variable region of an anti-kallikrein 1  
CC antibody of the invention.  
XX  
SQ Sequence 115 AA:  
Query Match 88.8%; Score 486, DB 10; Length 115;  
Best Local Similarity 87.7%; Pred. No. 2.5e-26;  
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDVVTITTCRAPOSISTYLNMYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 5 QMTQSPSSLSASVGDVVTITTCRAPOSISTYLNMYQOKPGKAPKLLIWSASNLQSGVPSRF 64  
QY 61 SGSGSGTEFTLTISNLQFEDPASYYCOQSYTTLTYTFGSGTKLEIKR 106  
DB 65 SGSGSGTEFTLTISNLQFEDPASYYCOQSYTTLTYTFGSGTKLEIKR 110  
RESULT 3  
AAR54260 standard; protein; 107 AA.  
XX  
AC AAR54260;  
XX  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)  
XX  
XX Anti-HIV gp120 immunoglobulin light chain variable region b22.  
XX  
DE  
XX  
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FRI  
FT Region 22..33

```

FT FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
FT
XX W09407922-A1.
XX
XX 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI, 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
XX gp41 and nucleic acid encoding them, useful for in vivo or in vitro
XX diagnosis and for passive immuno-therapy.
XX
XX Clatm 5; Page 189; 248bp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
XX using primers specific for heavy and light chain variable regions. The
XX amplification products were inserted into a digastronic vector to produce
XX a library of fragments. E.coli XL1 Blue cells were transformed with the
XX library. Filamentous phage were produced which expressed the Mab regions
XX on their surface. Panning with gp120 and gp41 resulted in the recovery of
XX immunoreactive clones. The light chain VK region sequence AARS4260
XX neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
XX
XX Sequence 107 AA;
SQ
Query Match 88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No.3.2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVTTTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGGSGGTFTLTISNLOPEDFASVYCOOSYTYLTGSGTKLEIKR 106
DB 61 SGGSGGTFTLTISNLOPEDFATVYCOOSYTYTYTGQTKLEIKR 106
RESULT 4
AAW01283
ID AAW01283 standard; protein; 107 AA.
XX
XX AAW01283;
XX
XX 29-JUN-1997 (first entry)
XX
XX VL region of HIV neutralising Mab, clone b22 and B35.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
XX HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
XX virus infectivity assay; precursor gp160; immunocompetence; human;
XX anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
FT
XX W09602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI, 1996-179601/18.
XX
XX Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
XX immuno-therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366bp; English.
XX
XX The sequences given in AAW01261-92 represent the light chain variable
XX regions (VL) of a series of monoclonal antibodies (Mab's) which are
XX immunoreactive with HIV glycoprotein gp120 and are capable of
XX neutralising HIV. This sequence represents the sequence of the Jk2 gene
XX clones, b22 and B35. A Mab containing this VL sequence has the capacity
XX to reduce HIV infectivity titre in an in vivo virus infectivity assay by
XX 50 % at a concentration of less than 700 ng of antibody/ml, and binds
XX mature gp120 preferentially over the precursor gp160. The Mab may be used
XX for determining immunocompetence of a human anti-HIV antibody and in the
XX detection of HIV infection
XX
XX Sequence 107 AA;
SQ
Query Match 88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No.3.2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDVTTTCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGGSGGTFTLTISNLOPEDFASVYCOOSYTYLTGSGTKLEIKR 106
DB 61 SGGSGGTFTLTISNLOPEDFATVYCOOSYTYTYTGQTKLEIKR 106
RESULT 5
AAV98244
ID AAV98244 standard; protein; 107 AA.
XX
XX AAV98244;
XX
XX 04-JUL-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone b22.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX

```

KM passive immunotherapy; reduce severity; HIV-induced disease;  
 KM immunocompetence; active immunisation.  
 XX  
 OS Homo sapiens.  
 XX AU948754-A.  
 XX  
 PD 17-FEB-2000.  
 XX  
 PF 16-SEP-1999; 99AU-00048754.  
 XX  
 PR 16-SEP-1999; 99AU-00048754.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Burton DR, Barbas CF, Lerner RA;  
 XX WPI; 2000-246867/22.  
 DR  
 XX  
 PT Human neutralizing monoclonal antibodies to human immunodeficiency virus  
 PT (HIV) used for providing passive immunotherapy to HIV are specific for  
 PT glycoprotein-120.

# Example 9, Fig 11, 374pp; English.

XX This sequence represents a fragment of the antibodies of the invention.  
 CC The invention relates to the production of an anti-HIV (human  
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable  
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity  
 CC assay by 50% at a concentration of less than 70 ng/mL. The method for the  
 CC production of the antibody comprises: (a) providing a first  
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence  
 CC (which does not comprise the sequence represented by AAY98206) and a  
 CC second polynucleotide encoding a light chain immunoglobulin amino acid  
 CC sequence; (b) inserting the first and second polynucleotide sequences  
 CC into a host cell; (c) maintaining the host cell in conditions which allow  
 CC the amino acid sequences encoded by the polynucleotides to be expressed  
 CC in the host cell; and (d) isolating the antibody comprising the heavy and  
 CC light chain immunoglobulin amino acid sequences from the host cell. The  
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive  
 CC immunotherapy to HIV in a human. They can be administered to high-risk  
 CC patients to reduce the likelihood and/or severity of HIV-induced disease  
 CC and to patients who are already HIV-infected. The antibodies are used for  
 CC neutralising field isolates which provides information about the  
 CC immunocompetence of an immune response in HIV patients, for detecting HIV  
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
 CC producing anti-idiotypic antibodies which can be used for active  
 CC immunisation and to screen human monoclonal antibodies to identify those  
 CC with the same binding specificity and to monitor the course of HIV  
 CC disease therapy by measuring the changes in concentration of HIV present  
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
 CC reduce the problems of significant host immune response to the antibodies  
 CC associated with monoclonal antibodies of xenogeneic or chimeric  
 CC derivation  
 XX  
 XX Sequence 107 AA;

SO Query Match 88.5%; Score 484; DB 3; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 3.2e-26;  
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCRASOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
 QY 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106  
 DB 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106

RESULT 6

AAY95135  
 ID AAY95135 standard; protein; 107 AA.  
 XX

AC AAY95135;  
 XX

DT 30-JUN-2000 (first entry)  
 XX

DE Anti-gp120 antibody light chain variable region from clone b22.  
 XX

KM Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;  
 KM reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;  
 KM glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.  
 XX

OS Homo sapiens.  
 XX

PN AU948756-A.  
 XX

PD 17-FEB-2000.  
 XX

PF 16-SEP-1999; 99AU-00048756.  
 XX

PR 16-SEP-1999; 99AU-00048756.  
 XX

PA (SCRI ) SCRIPPS RES INST.  
 XX

PI Burton DR, Barbas CF, Lerner RA;  
 XX

DR WPI; 2000-293393/26.  
 XX

PT Novel human monoclonal antibodies which immunoreact with and neutralize  
 PT human immunodeficiency virus useful for treating HIV infections.  
 XX

XX Example 9; Fig 11; 366pp; English.  
 XX

CC The present sequence represents a fragment of an anti-human  
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to  
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV  
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein  
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an  
 CC in vitro virus infectivity assay by 50%, at a concentration of less than  
 CC 700 ng/mL. The antibodies are used as reagents for the diagnosis and  
 CC immunotherapy of HIV induced disease. They are useful as neutralising  
 CC field isolates and provide useful information regarding the  
 CC immunocompetence of an immune response in HIV infected patients. The  
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies  
 CC which can be used to screen human monoclonal antibodies to identify  
 CC whether the antibody has the same binding specificity as the antibodies  
 CC of the invention. The neutralising antibodies define new epitopes on the  
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new  
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the  
 CC monoclonal antibodies derives from the fact that they are encoded by a  
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal  
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly  
 CC reduces the problems of significant host immune response to the passively  
 CC administered antibodies which is a problem commonly encountered when  
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.  
 CC An additional major advantage of the monoclonal antibodies described  
 CC derives from the fact that they immunoreact with a unique determinant  
 CC present on mature HIV glycoprotein gp120. This class of antibodies is  
 CC particularly effective at neutralising field isolates of HIV  
 XX  
 XX Sequence 107 AA;

SO Query Match 88.5%; Score 484; DB 3; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 3.2e-26;  
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
 DB 1 ELTQSPSSLSASVGDRTVITTCRASOSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
 QY 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106  
 DB 61 SGSSGTEFTLTISNLOFEDFASYYCOQSYTTLTYTGGSTKLEIKR 106

DB 61 SGGSGTDFLTITSLQPEDFATYYCOQSYSTPTFTGGTKLEIKR 106

## RESULT 7

AAAG93590  
ID AAAG93590 standard; protein; 107 AA.

AC AAAG93590;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) chain 102 protein sequence.

KM Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1;

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

(UNPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI: 2001-388931/41.

DR N-PSDB; AAH68647.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in

PT diagnostics requiring a human instead of an animal antibody and in

PT therapeutic medicine.

XX Claim 1; Col 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,

CC preferably a human antibody, (II) having an amino acid sequence comprising

CC one of the sequences (S) given in AAAG93558 to AAAG93669. (I) has

CC immunostimulant activity and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal

CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH6615 to AAH6726 represent the nucleotide sequence which encode

CC AAAG93558 to AAAG93669. AAAG93670 to AAAG93697 represent anti-Rh(D) heavy

CC chain CDR3 amino acid sequences which are given in the exemplification of

## RESULT 8

ABO27397  
ID ABO27397 standard; protein; 107 AA.

AC ABO27397;

XX 12-SEP-2003 (first entry)

DE Anti-Rh(D) chain 102.

KM Human; RH(D) binding protein; blood typing; blood product; antibody;

KW magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001, 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

(UNPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI: 2003-512273/48.

DR N-PSDB; ACD45311.

PT New human Rh(D)-binding protein useful for various diagnostic and

PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 26; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein

CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence

CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 107 AA;

XX Query Match 88.3%; Score 483; DB 6; Length 107;

XX Best Local Similarity 87.7%; Pred. No. 3.7e-26;

XX Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

XX 1 ELTQSPSSLSASVGDVVTITTCRASQISITLWYQKPGKAPKLLIWSASNLQGVPSRF 60

DB 2 ELTQSPSSLSASVGDVVTITTCRASQISITLWYQKPGKAPKLLIWSASNLQGVPSRF 61

QY 61 SGGSGTDFLTITSLQPEDFATYYCOQSYSTPTFTGGTKLEIKR 106

DB 62 SGGSGTDFLTITSLQPEDFATYYCOQSYSTPTFTGGTKLEIKR 107

DE Human anti-Rh(D) antibody clone SH13 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.  
 XX  
 PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2001-388931/41.  
 DR N-PSDB; AAH68701.  
 XX  
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in  
 PT diagnostics requiring a human instead of an animal antibody and in  
 PT therapeutic medicine.  
 XX  
 PS Claim 1; Col 68; 162pp; English.  
 XX  
 CC The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.  
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.  
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 4; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 6e-26; Indels 0; Gaps 0;  
 Matches 93; Conservative 9; Mismatches 4;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDVVTITTCRAQSISTYLMWYQKPKAPKLLIWAASLSRSGVPSRF 61  
 QY 61 SGGSGSGTEFTLTITSNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
 DB 62 SGGSGSGTDFLTITSLQPEDFATYYCOQSYSTPYTFGQGTLEIKR 107

RESULT 10  
 ABO27451  
 ID ABO27451 standard; protein; 107 AA.  
 XX  
 AC ABO27451;

DT 12-SEP-2003 (first entry)  
 DE Anti-Rh(D) light chain SH13.  
 XX

KM Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KM magnetically activated cell sorting.  
 XX

OS Homo sapiens.  
 XX

PN US2003040605-A1.  
 XX

PD 27-FEB-2003.  
 XX

PF 04-MAY-2001; 2001US-00848798.  
 XX

PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX

PA (UYPE-) UNIV PENNSYLVANIA.  
 XX

XX  
 PI Siegel DL;  
 XX  
 DR WPI; 2003-512273/48.  
 DR N-PSDB; ACD45365.  
 XX  
 PT New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.  
 XX  
 PS Claim 4; Page 50; 187pp; English.  
 XX  
 CC The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain  
 XX  
 SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 6; Length 107;  
 Best Local Similarity 87.7%; Pred. No. 6e-26; Indels 0; Gaps 0;  
 Matches 93; Conservative 9; Mismatches 4;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60  
 DB 2 ELTQSPSSLSASVGDVVTITTCRAQSISTYLMWYQKPKAPKLLIWAASLSRSGVPSRF 61  
 QY 61 SGGSGSGTEFTLTITSNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
 DB 62 SGGSGSGTDFLTITSLQPEDFATYYCOQSYSTPYTFGQGTLEIKR 107

RESULT 11  
 AEE74528  
 ID AEE74528 standard; protein; 107 AA.  
 XX  
 AC AEE74528;

DT 23-FEB-2006 (first entry)  
 DE Anti-Rh(D) light chain SH13, SEQ ID 156.  
 XX

KM Rh(D); erythrocyte; tissue typing; transplantation; light chain.  
 KM Synthetic.  
 XX

OS Synthetic.  
 XX

PN US2005282252-A1.  
 XX

PD 22-DEC-2005.  
 XX

PF 22-FEB-2005; 2005US-00064174.  
 XX

PR 11-OCT-1996; 96US-0028550P.  
 PR 27-JUN-1997; 97US-00884045.  
 PR 10-APR-1998; 98US-0081380P.  
 PR 29-JAN-1999; 99US-00240274.  
 XX

PA (SIEG/) SIEGEL D L.  
 XX

PI Siegel DL;  
 XX

DR WPI; 2006-046435/05.  
 DR N-PSDB; AEE74571.  
 XX

PT New RH(D)-binding proteins, useful for typing donor white blood cells for  
 PT human leukocyte antigens for the purposes of matching donors and  
 PT recipients for potential transplant matching in the case of both solid  
 PT organ or tissue transplanting.  
 XX

PS Claim 5; SEQ ID NO 156; 99pp; English.  
 XX

CC The present invention relates to novel Rh(D) antibody light and heavy  
 CC chains. The antibody heavy chains are given in AEE74373-AEE74400 and



CC ABE74511-ABE74525. The antibody light chains are given in ABE74398-  
CC ABE74441 and ABE74526-ABE74553. The Rh(D) antigen is a red blood cell  
CC membrane protein. The antibodies are useful for typing donor white blood  
CC cells for human leukocyte antigen (HLA) antigens for the purposes of  
CC matching donors and recipients for potential transplant matching in the  
CC case of both solid (for example, kidney, heart, liver, lung) and non-  
CC solid (for example, bone marrow) organ or tissue transplanting. The  
CC present sequence is one such antibody light chain.  
XX  
SQ Sequence 107 AA:  
Query Match 87.8%; Score 480; DB 10; Length 107;  
Best Local Similarity 87.7%; Pred. No. 6e-26;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLMVYQOKPGKAPKLLWMSASNLOSQVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTTCRAROSISTYLMVYQOKPGKAPKLLWMSASNLOSQVPSRF 61  
QY 61 SGSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGTGKLEIKR 106  
DB 62 SGSGSGTDFTLTISNLOFEDFATYTCQOSYSTVTTGCGTKLEIKR 107  
DE  
RESULT 12  
ID AEG01281 standard; protein; 115 AA.  
XX AEG01281;  
AC  
XX  
XX  
DT 20-APR-2006 (first entry)  
XX  
XX  
DE Kallikrein 1 antibody light chain variable region SEQ ID NO:1108.  
XX  
XX  
KW Antibody; light chain variable region; kallikrein 1; therapeutic;  
KW Antiasthmatic; Respiratory-Gen.; Neuroprotective; Antipsoriatic;  
KW Antineumatic; Antiarthritic; Osteopathic; Antiallergic;  
KW Antiinflammatory; Gastrointestinal-Gen.; Antidiabetic; Cytostatic;  
KW Cardiovascular-Gen.; uropathic; Angiogenesis inhibitor; asthma;  
KW Chronic obstructive pulmonary disease; multiple sclerosis; psoriasis;  
KW Rheumatoid arthritis; osteoarthritis; allergic rhinitis; sinusitis;  
KW Inflammatory bowel disease; diabetes; pancreatitis;  
KW Interstitial cystitis; neoplasm; pancreatic ductal adenocarcinoma; tumor;  
KW angiogenesis; cardiovascular disease.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO2006017538-A2.  
XX  
XX  
PD 16-FEB-2006.  
XX  
XX  
PF 03-AUG-2005; 2005WO-US027493.  
XX  
XX  
PR 03-AUG-2004; 2004US-0598506P.  
XX  
XX  
PR 04-OCT-2004; 2004US-0615721P.  
XX  
XX  
PA (DYAX-) DYAX CORP.  
XX  
XX  
PI Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q;  
XX  
XX  
DR WPI; 2006-184027/19.  
XX  
XX  
PT Novel protein comprising immunoglobulin heavy and light chain variable  
PT domain sequences, capable of inhibiting human tissue Kallikrein-1  
PT enzymatic activity, useful for treating human tissue Kallikrein-1  
PT associated disorder, e.g. asthma.  
XX  
XX  
PS Example; SEQ ID NO 1108; 178pp; English.  
XX  
XX  
CC The invention relates to a protein (I) comprising an immunoglobulin heavy  
CC chain (HC) variable domain sequence and an immunoglobulin light chain  
CC (LC) variable domain sequence, where the HC variable domain sequence and  
CC the LC variable domain sequence form an antigen binding site binding to

CC human tissue kallikrein-1 (hK1) and inhibit enzymatic activity of hK1.  
CC Also included is a pharmaceutical composition (II) comprising the protein  
CC and carrier. The protein is useful for treating or preventing an hK1  
CC associated disorder, which involves administering (I) to a subject to  
CC treat or prevent the hK1 associated disorder. The disorder is chosen from  
CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,  
CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,  
CC inflammatory bowel diseases, immune mediated diabetes, acute  
CC pancreatitis, interstitial cystitis or neoplastic disorder. The disorder  
CC is asthma and the asthma is allergic or non-allergic asthma. The disorder  
CC is a neoplastic disorder, which is metastatic pancreatic adenocarcinoma  
CC or tumor angiogenesis. The method further involves administering a second  
CC agent that modulates angiogenesis. The second agent is an anti-vascular  
CC endothelial growth factor (VEGF) antibody or its antigen binding  
CC fragment. The protein is useful for modulating an hK1 activity, for  
CC detecting the presence of an hK1 protein in vitro, for detecting the  
CC presence of an hK1 in vivo in a human subject, and for reducing the  
CC angiogenesis associated with cardiovascular disorders. The present  
CC sequence is the light chain variable region of an anti-kallikrein 1  
CC antibody of the invention.  
XX  
SQ Sequence 115 AA:  
Query Match 87.4%; Score 478; DB 10; Length 115;  
Best Local Similarity 86.8%; Pred. No. 8.7e-26;  
Matches 92; Conservative 10; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLMVYQOKPGKAPKLLWMSASNLOSQVPSRF 60  
DB 5 QMTQSPSSLSASVGDVVTTCRAROSISTYLMVYQOKPGKAPKLLWMSASNLOSQVPSRF 64  
QY 61 SGSGSGTEFTLTISNLOFEDFASVYCOQSYTTLTYTSGTGKLEIKR 106  
DB 65 SGSGSGTDFTLTISNLOFEDFATYTCQOSYSTVTTGCGTKLEIKR 110  
DE  
RESULT 13  
ID AAR54261 standard; protein; 107 AA.  
XX AAR54261;  
AC  
XX  
XX  
DT 25-MAR-2003 (revised)  
DT 10-NOV-1994 (first entry)  
XX  
XX  
DE Anti-HIV gp120 immunoglobulin light chain variable region b27.  
XX  
XX  
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;  
KW neutralisation; monoclonal antibody; kappa light chain; variable region;  
KW framework; complementarity determining region.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..21  
FT /label= FR1  
FT Region 22..33  
FT /label= CDR1  
FT Region 34..48  
FT /label= FR2  
FT 49..55  
FT /label= CDR2  
FT 56..87  
FT /label= FR3  
FT Region 88..95  
FT /label= CDR3  
FT 96..107  
FT /label= FR4  
XX  
XX  
PN WO9407922-A1.  
XX  
XX  
XX  
PD 14-APR-1994.  
XX

```

PF 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Claim 5; Page 190; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the Mab regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AKS4261.
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct FN field.)
XX
XX Sequence 107 AA;
SQ
Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,1e-25;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPKAPKLLIWAASLQSGVPSRF 60
QY 61 SSGSGSTFTLTITSNLOFEDFPASYCOOSYTTLYTFSGTKLEIKR 106
DB 61 SSGSGSTFTLTITSNLOFEDFPASYCOOSYTTLYTFSGTKLEIKR 106

RESULT 14
AAW01284
ID AAW01284 standard; protein; 107 AA.
XX
XX AAW01284;
XX
XX 29-JAN-1997 (first entry)
XX
XX VL region of HIV neutralising Mab, clone B27.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
KM HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KM anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..21
FT /label= FR1
FT 22..32
FT /label= CDRI
FT 33..47
FT /label= FR2
FT 48..54
FT /label= CDR2
FT 55..86
FT /label= FR3
FT 87..95
FT /label= CDR3
FT 96..107
FT /label= FR4
XX

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PN W09602273-A1.
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in passive
PT immuno-therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366pp; English.
XX
XX The sequences given in AAW01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the VK2 gene
CC clone, B27. A Mab containing this VL sequence has the capacity to reduce
CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a
CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
CC preferentially over the precursor gp160. The Mab may be used for
CC determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
XX
XX Sequence 107 AA;
SQ
Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1,1e-25;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPKAPKLLIWAASLQSGVPSRF 60
QY 61 SSGSGSTFTLTITSNLOFEDFPASYCOOSYTTLYTFSGTKLEIKR 106
DB 61 SSGSGSTFTLTITSNLOFEDFPASYCOOSYTTLYTFSGTKLEIKR 106

RESULT 15
AAV98245
ID AAV98245 standard; protein; 107 AA.
XX
XX AAV98245;
XX
XX 04-JUL-2000 (first entry)
XX
XX Anti-gp120 antibody light chain variable region from clone B27.
XX
XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KM human immunodeficiency virus type 1; HIV-1; infectivity titre;
KM passive immunotherapy; reduce severity; HIV-induced disease;
KM immunocompetence; active immunisation.
XX
XX Homo sapiens.
XX
XX AAV98245-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX

```

XX WPI: 2000-246867/22.

DR Human neutralizing monoclonal antibodies to human immunodeficiency virus  
XX (HIV) used for providing passive immunotherapy to HIV are specific for  
PT glycoprotein-120.  
PS  
XX

PS Example 9; Fig 11; 374p; English.

XX This sequence represents a fragment of the antibodies of the invention.  
CC The invention relates to the production of an anti-HIV (human  
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable  
CC of reducing an HIV infectivity titre in an in vitro virus infectivity  
CC assay by 50% at a concentration of less than 70 ng/ml. The method for the  
CC production of the antibody comprises: (a) providing a first  
CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence  
CC .which does not comprise the sequence represented by AA196206) and a  
CC second polynucleotide encoding a light chain immunoglobulin amino acid  
CC sequence; (b) inserting the first and second polynucleotide sequences  
CC into a host cell; (c) maintaining the host cell in conditions which allow  
CC the amino acid sequences encoded by the polynucleotides to be expressed  
CC in the host cell; and (d) isolating the antibody comprising the heavy and  
CC light chain immunoglobulin amino acid sequences from the host cell. The  
CC anti-HIV gp-120 monoclonal antibody is used for providing passive  
CC immunotherapy to HIV in a human. They can be administered to high-risk  
CC patients to reduce the likelihood and/or severity of HIV-induced disease  
CC and to patients who are already HIV-infected. The antibodies are used for  
CC neutralising field isolates which provides information about the  
CC immunocompetence of an immune response in HIV patients, for detecting HIV  
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for  
CC producing anti-idiotypic antibodies which can be used for active  
CC immunisation and to screen human monoclonal antibodies to identify those  
CC with the same binding specificity and to monitor the course of HIV  
CC disease therapy by measuring the changes in concentration of HIV present  
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120  
CC monoclonal antibodies are encoded by a human polynucleotide sequence and  
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease  
CC reduce the problems of significant host immune response to the antibodies  
CC associated with monoclonal antibodies of xenogeneic or chimeric  
CC derivation  
XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;

Best Local Similarity 87.7%; Pred. No. 1,1e-25; Mismatches 5; Indels 0; Gaps 0;

Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTITTCRAQGISITLYLWYQKPGKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGRVTITTCRAQGISITLYLWYQKPGKAPKLLIWSASNLQGVPSRF 60  
QY 61 SSGSGSTERTLTITSNLQFEDFASYCOQSYTTLTYTGSGTKLEIKR 106  
DB 61 SSGSGSTERTLTITSNLQFEDFASYCOQSYTTLTYTGSGTKLEIKR 106

Search completed: August 30, 2006, 00:41:46  
Job time : 97.2394 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 9.95758 Seconds  
(without alignments)  
1024.243 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547  
Sequence: 1 ELTQSPSSLSASVGVDRVTIT.....QOSYTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	85.6	108	2 B49047	Ig kappa chain V r
2	465	85.0	127	2 S47182	Ig kappa chain - h
3	465	85.0	127	2 S40367	Ig kappa chain V-J
4	464	84.8	109	2 S31998	Ig kappa chain - h
5	462	84.5	123	2 S40331	Ig kappa chain - h
6	457	83.5	122	2 S40370	Ig kappa chain - h
7	455	83.2	108	2 S44122	Ig kappa chain V r
8	454	83.0	108	2 S31977	Ig kappa chain - h
9	453	82.8	129	1 K1H0WK	Ig kappa chain pre
10	451	82.4	109	2 S31981	Ig kappa chain - h
11	451	82.4	109	2 S31978	Ig kappa chain - h
12	449	82.1	108	1 K1H0DE	Ig kappa chain V-I
13	447	81.7	129	2 S19674	Ig kappa chain V r
14	446	81.5	108	2 S40317	Ig kappa chain - h
15	438	80.1	117	2 S46371	Ig kappa chain V-J
16	437.5	80.0	106	2 PC2624	Ig kappa chain V
17	437	79.9	107	2 S36264	Ig lambda chain V
18	437	79.9	108	1 K1H0HU	Ig kappa chain V-I
19	437	79.9	120	2 S46370	Ig kappa chain V-J
20	436	79.7	109	2 S31979	Ig kappa chain - h
21	434	79.3	129	2 S52793	Ig kappa chain V r
22	432	79.2	128	2 S46372	Ig kappa chain V r
23	432	79.0	109	2 S31980	Ig kappa chain - h
24	432	79.0	125	2 S40350	Ig kappa chain - h
25	431	78.8	109	2 S31983	Ig kappa chain - h
26	429	78.4	129	2 S52792	Ig kappa chain V r
27	429	78.4	132	2 S40334	Ig kappa chain - h
28	428	78.2	109	2 S32001	Ig kappa chain - h
29	428	78.2	122	2 S40314	Ig kappa chain - h

30	428	78.2	132	2 S38646	Ig kappa chain V r
31	427.5	78.2	125	2 S40315	Ig kappa chain - h
32	427	78.1	125	2 S40349	Ig kappa chain V-J
33	425.5	77.8	124	2 S40336	Ig kappa chain V-J
34	424.5	77.6	107	2 S36275	Ig lambda chain V
35	424	77.5	108	1 K1H0U	Ig kappa chain V-I
36	424	77.5	125	2 S40333	Ig kappa chain V-J
37	421.5	77.1	108	2 S30521	Ig kappa chain V r
38	419	76.6	117	2 A27594	Ig kappa chain pre
39	419	76.6	116	2 S24206	Ig kappa chain V r
40	418	76.4	109	2 JN0296	Ig kappa chain V-J
41	418	76.4	129	2 S40369	Ig kappa chain - h
42	417.5	76.3	108	2 S34007	Ig kappa chain V r
43	417	76.2	126	2 S40335	Ig kappa chain V-J
44	416	76.1	108	1 K1H0U	Ig kappa chain V-I
45	416	76.1	108	1 K1H0RE	Ig kappa chain V-I

#### ALIGNMENTS

##### RESULT 1

B49047  
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: B49047  
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lemon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A/Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
A/Reference number: A49047; MUID:92387224; PMID:1516616  
A/Accession: B49047  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-108 <VIC>  
A/References: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44  
A/Experimental source: thymic B lymphocytes  
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBI:P.113209)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match 85.6%; Score 468; DB 2; Length 108;  
Best Local Similarity 84.9%; Pred. No. 3.8e-34;  
Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGVDRVTITCRAROSITRYLMWYQOKPKAPKLTIMASNLQSGVPSRF 60  
:::|||||  
Db 3 QMTQSPSSLSASVGVDRVTITCRASOSISRYLMWYQOKPKAPKLTIVAASSLQSGVPSRF 62  
OY 61 SGSGSGTEFTLTISNLPEDFASVYCCQOSYTLTYFGSGTKLEIKR 106  
|||||  
Db 63 SGSGSGTDTLTITSSLPEDFATYCCQOSYSLPRTGCGTKVEIKR 108

##### RESULT 2

S47182  
Ig kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
R/McInosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
C/Accession: S47182  
Submitted to the EMBL Data Library, June 1994  
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient  
A/Reference number: S47181  
A/Accession: S47182  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-108 <WCI>  
C/Cross-references: UNIPARC:UPI0000116185; EMBL:X79786; NID:G506422; PTDN:CA56182.1; PII  
C/Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMW>

```
Query Match      85.0%; Score 465; DB 2; Length 108;
Best Local Similarity 85.8%; Pred. No. 6, 3e-34;
Matches 91; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ELTQSPSSLSASVGDVVTTCRASQSSISYLMWYQKPGKAPKLLIYAASLSQGVPSRF 62
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGGTEFTLTISNLOPEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGGSGGTEFTLTISNLOPEDFATYCCOQSYTPTSGGTRLEIKR 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Status: preliminary; translation not shown
A/Accession: S40367
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
A/Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match      85.0%; Score 465; DB 2; Length 127;
Best Local Similarity 84.0%; Pred. No. 8, 1e-34;
Matches 89; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QMTQSPSSLSASVGDVVTTCRASQSSISYLMWYQKPGKAPKLLIYAASLSQGVPSRF 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGGTEFTLTISNLOPEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SGGSGGTEFTLTISNLOPEDFATYCCOQSYTPTFGGTRLEIKR 125
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S31998
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:938501; PIDN:CAA78790.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match      84.8%; Score 464; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 8, 5e-34;
Matches 90; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGRVTTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 MTQSPSSLSASVGRVTTTCRASQSSISYLMWYQKPGKAPKLLIYAASLSQGVPSRF 63
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 GSGSGTEFTLTISNLOPEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 64 GSGSGTEFTLTISNLOPEDFATYCCOQSYDTPWTFGGTRLEIKR 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Accession: S40331
A/Molecule type: mRNA
A/Residues: 1-123 <KLE>
A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match      84.5%; Score 462; DB 2; Length 123;
Best Local Similarity 84.8%; Pred. No. 1, 4e-33;
Matches 89; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 QMTQSPSSLSASVGDVVTTCRASQSSISYLMWYQKPGKAPKLLIYAASLSQGVPSRF 78
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGGTEFTLTISNLOPEDFASYCCOQSYTTLTYFGSGTKLEIKR 105
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 SGGSGGTEFTLTISNLOPEDFATYCCOQSYTPTFGGTRLEIKR 123
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S40370
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40370
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40370
A/Status: preliminary; translation not shown
A/Accession: S40370
A/Molecule type: mRNA
A/Residues: 1-122 <KLE>
A/Cross-references: UNIPARC:UPI0000116178; EMBL:X72480; NID:9441428; PIDN:CAA51148.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/30-104/Domain: immunoglobulin homology <IMM>

Query Match      83.5%; Score 457; DB 2; Length 122;
Best Local Similarity 84.9%; Pred. No. 3, 9e-33;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 QLTQSPSSLSASVGDVVTTCRASQSSISTFLHWYQKPGKAPKLLIYAASNLQGVPSRF 76
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGGTEFTLTISNLOPEDFASYCCOQSYTTLTYFGSGTKLEIKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 SGGSGGTEFTLTISNLOPEDFATYCCOQSYTPTFGGTRLEIKR 122
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S44122
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
```

Accession: S44122  
R:Hacking, R.E.; Zhu, D.; Orecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable r  
A:Reference number: S44105  
A:Accession: S44122  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-108 <HAM>  
A:Cross-References: UNIPARC:UPI0000116630; EMBL:Z31390; NID:g472976; PIDN:CAAB3265.1; PR  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 455; DB 2; Length 108;  
Best Local Similarity 84.0%; Pred. No. 5.1e-33;  
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDVRVITTCRAQSISTYLNWYQOKGKAPKLLIWSASNIQGVPSRF 60  
D 3 QMTQSSPSLSASVGDVRVITTCRAQSISTYLNWYQOKGKAPKLLIWSASNIQGVPSRF 62  
QY 61 SGSSSGTPEFTLITISLQPEDFASYYCOQSYTTLTFPGSGTLEIKR 106  
D 63 SGSSSGTPEFTLITISLQPEDFALYYCOQSYTTPWTFGGTKEIKR 108

RESULT 8  
S31977  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
A:Accession: S31977  
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; Mclachlan, S.M.; Rapoport, B.  
submitted to the EMBL Data Library, June 1992  
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as  
A:Reference number: S31977  
A:Accession: S31977  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-108 <POR>  
A:Cross-References: UNIPROT:O96S49; UNIPARC:UPI0000176B27; EMBL:Z15073  
C:Superfamily: immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 454; DB 2; Length 108;  
Best Local Similarity 84.8%; Pred. No. 6.2e-33;  
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDVRVITTCRAQSISTYLNWYQOKGKAPKLLIWSASNIQGVPSRF 61  
D 4 MTQSSPSLSASVGDVRVITTCRAQSISTYLNWYQOKGKAPKLLIWSASNIQGVPSRF 63  
QY 62 GSGSGTPEFTLITISLQPEDFASYYCOQSYTTLTFPGSGTLEIKR 106  
D 64 GSGSGTPEFTLITISLQPEDFALYYCOQSYTTPWTFGGTKEIKR 108

RESULT 9  
K1HWK  
Ig kappa chain precursor V-J region (Walker) - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
A:Accession: A01883  
R:Klobeck, H.G.; Combratio, G.; Zachau, H.G.  
Nucleic Acids Res. 12, 6995-7006, 1984  
A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell  
A:Reference number: A93534; MUID:85014148; PMID:6091049  
A:Accession: A01883  
A:Molecule type: DNA  
A:Residues: 1-129 <KLO>  
A:Cross-References: UNIPROT:P04431; UNIPARC:UPI0000012E151

A>Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-2/2/Domain: signal sequence #status predicted <SIG>

F:123-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAY>

F:138-112/Domain: immunoglobulin homology <IMM>

F:146-56/Region: complementarity-determining 1

F:157-71/Region: framework 2

F:172-78/Region: complementarity-determining 2

F:179-110/Region: framework 3

F:111-119/Region: complementarity-determining 3

F:1120-129/Region: framework 4

F:45-110/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 82.8%; Score 453; DB 1; Length 129;

Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 LTQSPSSLSASVGDVRVITTCRAQGISITVLMWYQKPKGAPKLLIWSASNLQGVPSRF 60

DB 25 QMTQSPSSLSASVGDVRVITTCRAQGISITVLMWYQKPKGAPKLLIWSASNLQGVTSRF 84

QY 61 SGGSGTFTLTISNLOFEDPASVYCCQGSYTLTYTFGSGTKLEIK 105

DB 85 SGGSGTFTLTISNLOFEDPASVYCCQGSYTLTYTFGSGTKLEIK 129

RESULT 10

S31981

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S31981

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McClachlan, S.M.; Rapoport, B. Submitted to the EMBL Data Library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as A:Reference number: S31977

A:Accession: S31981

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <PDB>

A:Cross-references: UNIPARC:UPI0000116494; EMBL:215077; NID:g38493; PIDN:CAA78786.1; PID: C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.4%; Score 451; DB 2; Length 109;

Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDVRVITTCRAQGISITVLMWYQKPKGAPKLLIWSASNLQGVPSRF 61

DB 4 MTQSPSSLSASVGRVITTCRAQGISITVLMWYQKPKGAPKLLIWSASNLQGVTSRF 63

QY 62 GSGSGTFTLTISNLOFEDPASVYCCQGSYTLTYTFGSGTKLEIK 106

DB 64 GSGSGTFTLTISNLOFEDPASVYCCQGSYTLTYTFGSGTKLEIK 108

RESULT 11

S31978

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S31978

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McClachlan, S.M.; Rapoport, B.

submitted to the EMBL Data Library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

A:Reference number: S31577

A:Accession: S31578

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <PDB>

A:Cross-references: UNIPARC:UPI0000116491; EMBL:Z15074; NID:938487; PIDN:CAA78783.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;

Best Local Similarity 82.9%; Pred. No. 1.2e-32;

Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

2 LTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61

4 LTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 63

62 GSGSGTEFTLTISNLOPEDFASVYCOQSYTTLVTFSGTKLEIKR 106

64 GSGSGTDFLTITSLQPEDFATYVCOQSYTTPYTFGGTKLEIKR 108

RESULT 12

IG kappa chain V-I region (Dee) - human (tentative sequence)

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004

C:Accession: A01865

R:Milstein, C.P.; Deverson, E.V.

Biochem. J. 123, 945-958, 1971

A:Title: The amino acid sequence of a human kappa light chain.

A:Reference number: A01865; PMID:7205133; PMID:5124336

A:Accession: A01865

A:Molecule type: protein

A:Residues: 1-108 <ML>

A:Cross-references: UNIPROT:P01597; UNIPARC:UPI000012E141

A>Note: the C region of this chain as the Inv (3) marker

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-86/Disulfide bonds: #status predicted

Query Match 82.1%; Score 449; DB 1; Length 108;

Best Local Similarity 80.2%; Pred. No. 1.7e-32;

Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

3 ZMTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 62

61 GSGSGTEFTLTISNLOPEDFASVYCOQSYTTLVTFSGTKLEIKR 106

63 GSGSGTDFLTITSLQPEDFATYVCOQSYTTPYTFGGTKLEIKR 108

RESULT 13

IG kappa chain V region (clone alpha-TEL9) - human

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000

C:Accession: S19674

R:Mark, U.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,

J. Mol. Biol. 222, 581-597, 1991

A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph

A:Reference number: S19663; PMID:92085276; PMID:1748994

A:Accession: S19674

A:Molecule type: mRNA

A:Residues: 1-108 <MAR>

A:Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:937860; PIDN:CAA43823.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 447; DB 2; Length 108;

Best Local Similarity 83.8%; Pred. No. 2.5e-32;

Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

2 LTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61

4 LTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 63

62 GSGSGTEFTLTISNLOPEDFASVYCOQSYTTLVTFSGTKLEIKR 106

64 GSGSGTDFLTITSLQPEDFATYVCOQSYTTPYTFGGTKLEIKR 108

RESULT 14

IG kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40317

R:Klein, R.; Jelenchen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin ch1 genes and their hypermutation.

A:Reference number: S40312; PMID:94080891; PMID:8258341

A:Accession: S40317

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-129 <KLE>

A:Cross-references: UNIPARC:UPI0000116143; EMBL:X72427; NID:9441322; PIDN:CAA51095.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:37-11/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 446; DB 2; Length 129;

Best Local Similarity 81.0%; Pred. No. 3.7e-32;

Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

1 ELTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

24 QMTQSPSSLSASVGDVVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 83

61 GSGSGTEFTLTISNLOPEDFASVYCOQSYTTLVTFSGTKLEIKR 105

84 GSGSGTDFLTITSLQPEDFATYVCOQSYTTPYTFGGTKLEIKR 128

RESULT 15

IG kappa chain V-J region (T24-3) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C:Accession: S46371; S38645

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reat

A:Reference number: S46369; PMID:94313975; PMID:8039491

A:Accession: S46371

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: UNIPARC:UPI0000116544; EMBL:Z27172; NID:9415959; PIDN:CAA81696.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 438; DB 2; Length 117;





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Wed Aug 30 10:03:30 2006

us-10-027-725a-11.rup

Page 1

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 57.8182 Seconds

(without alignments)  
1695.862 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547

Sequence: 1 ERTQSPSSLSASVGRVIT.....QQSYTTLVTFSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt\_7.2.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	85.4	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
2	465.5	85.1	107	2 Q6SAS9_HUMAN	Q6SAS9 homo sapien
3	463	82.8	129	1 KV1B_HUMAN	P04431 homo sapien
4	449	82.1	108	1 KV1B_HUMAN	P01577 homo sapien
5	448.5	82.0	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
6	437	79.9	108	1 KV1H_HUMAN	P01600 homo sapien
7	433	79.2	236	2 Q6GKX8_HUMAN	Q6GKX8 homo sapien
8	431	78.8	236	2 Q6GKX0_HUMAN	Q6GKX0 homo sapien
9	430	78.6	236	2 Q6GKX0_HUMAN	Q6GKX0 homo sapien
10	428	78.2	236	2 Q6PIH7_HUMAN	Q6PIH7 homo sapien
11	424	77.5	108	1 KV1N_HUMAN	P01606 homo sapien
12	423	77.3	234	2 Q72473_HUMAN	Q72473 homo sapien
13	416	76.1	108	1 KV1B_HUMAN	P01594 homo sapien
14	416	76.1	108	1 KV1O_HUMAN	P01607 homo sapien
15	414	75.7	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
16	413.5	75.6	107	1 KV1D_HUMAN	P01596 homo sapien
17	413	75.5	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien
18	412	75.3	129	1 KV1X_HUMAN	P04432 homo sapien
19	411.5	75.2	109	1 KV1T_HUMAN	P01612 homo sapien
20	411	75.1	108	1 KV1S_HUMAN	P01611 homo sapien
21	408	74.6	108	1 KV1V_HUMAN	P04430 homo sapien
22	408	74.6	236	2 Q723Y4_HUMAN	Q723Y4 homo sapien
23	407	74.4	108	1 KV1E_HUMAN	P01598 homo sapien
24	405	74.0	236	2 Q502W4_HUMAN	Q502W4 homo sapien
25	403	73.7	108	1 KV1P_HUMAN	P01608 homo sapien
26	402	73.5	108	1 KV1G_HUMAN	P01593 homo sapien
27	402	73.5	108	1 KV1G_HUMAN	P01599 homo sapien
28	401	73.3	108	1 KV1L_HUMAN	P01604 homo sapien
29	401	73.3	108	1 KV1Y_HUMAN	P80362 homo sapien
30	401	73.3	234	2 Q5EF66_HUMAN	Q5EF66 homo sapien
31	401	73.3	236	2 Q6P1T5_HUMAN	Q6P1T5 homo sapien

32	399	72.9	108	1 KV1R_HUMAN	P01610 homo sapien
33	398	72.8	189	2 Q56917_HUMAN	Q56917 homo sapien
34	398	72.8	236	2 Q6GKX9_HUMAN	Q6GKX9 homo sapien
35	397	72.6	244	2 Q65ZC8_HUMAN	Q65ZC8 homo sapien
36	396	72.4	108	1 KV1C_HUMAN	P01595 homo sapien
37	395	72.2	108	1 KV1M_HUMAN	P01605 homo sapien
38	395	72.2	236	2 Q6PIH4_HUMAN	Q6PIH4 homo sapien
39	394	72.0	240	2 Q65ZC9_HUMAN	Q65ZC9 homo sapien
40	393	71.8	108	1 KV1K_HUMAN	P01603 homo sapien
41	384	70.2	108	1 KV1Q_HUMAN	P01609 homo sapien
42	384	70.2	108	1 KV1S_MOUSE	P01646 mus musculu
43	383	70.0	117	1 KV1J_HUMAN	P01602 homo sapien
44	377	68.9	117	1 KV1I_HUMAN	P01601 homo sapien
45	375	68.6	108	1 KV5N_MOUSE	P01647 mus musculu

## ALIGNMENTS

RESULT 1  
Q9UL77\_HUMAN PRELIMINARY; PRT; 108 AA.  
ID Q9UL77\_HUMAN  
AC Q9UL77;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92387224; PubMed=1516616;  
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
RT "Human monoclonal strational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autolimmune repertoire".  
RT Eur. J. Immunol. 22:2231-2236(1992).  
RL [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93170387; PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation".  
RT Eur. J. Immunol. 23:391-397(1993).  
RL [4]  
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CC EMBL, AF035037; AAD56273.1; -; mRNA.  
CC PIR; B49047; B49047.  
CC PIR; S34083; S34083.  
CC HSSP; P01607; 1BMW.  
CC SMR; Q9UL77; 1-108.  
CC Ensemble; ENSG00000163245; Homo sapiens.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003596; IG V.  
CC InterPro; IPR013106; V-set.  
CC SMART; SM00409; IG\_1.  
CC SMART; SM00406; IGV\_1.  
CC PROSITE; PS50835; IG\_LIKE; 1.

KM Immunoglobulin domain.  
 FT NON\_TER 1 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11738 MW; C0668176C4D16F3 CRC64;  
 Query Match 85.4%; Score 467; DB 2; Length 108;  
 Best Local Similarity 84.0%; Pred. No. 1,7e-41;  
 Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0.

QY 1 ELTQSPSSLSASVGDVVTITCRARQISITYLNMVQKQKPKLLIWSASINSQVPSRF 60  
 DB 3 QMTQSPSSLSASVGVRTVITCRASQISISYLNWYQKQKAPNLLIYAASSLSQGVPSRF 62  
 QY 61 SGSSGTEFTLTISLQFEDFASYYCOQSYTLTYRFGSGTKLEIKR 106  
 DB 63 SGSSGTDFTLTISLQFEDFATYYCOQSYSTSTWTFGKVEIKR 108

RESULT 2  
 Q96SA9\_HUMAN  
 ID Q96SA9\_HUMAN PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9\_1  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 18.  
 DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglycosamine/anti-mysin  
 RT antibody V region genes.";  
 RL J. Immunol. 161:2020-2031(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92387224; PubMed=1516616;  
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
 RT "Human monoclonal strictional autoantibodies isolated from thymic B  
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
 RT segments associated with the autoimmune repertoire.";  
 RL Eur. J. Immunol. 22:2231-2236(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93170387; PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation.";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;  
 RA Mahelner-Lory A., Katz J.B., Pillingner M., Ghosein C., Smith A.,  
 RA Diamond B.;  
 RT "Molecular characteristics of antibodies bearing an anti-DNA-  
 RT associated idiotype.";  
 RL J. Exp. Med. 174:1639-1652(1991).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91243737; PubMed=1903706;  
 RA Blaison G., Kuntz J.L., Pasquali J.L.;  
 RT "Molecular analysis of V kappa III variable regions of polyclonal  
 RT rheumatoid factors during rheumatoid arthritis.";  
 RL Eur. J. Immunol. 21:1221-1227(1991).

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CC EMBL, U96396; AAB68785.1; -, mRNA.
CC
DR PIR, B49047; B49047.
DR PIR, PH0867; PH0867.
DR PIR, S16840; S16840.
DR PIR, S31977; S31977.
DR PIR, S34083; S34083.
DR PIR, S34086; S34086.
DR HSSP, P01607; 1BMW.
DR SMR, Q96SA9; 1-107.
DR Ensembl, ENSG00000163245; Homo sapiens.
DR LinkHub; Q96SA9; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT TER 1
FT SEQUENCE 107 AA; 107 MW; 4BB43E9C5B577F16 CRC64;
SQ
Query Match 85.1%; Score 465.5; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.4e-41;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;
QY 1 ELTQSPSSLSAVGDRVITITTRAGOSISTYLNWYQQRGKAPKLLIMASNLQSGVPSRF 60
DB 3 QMTQSPSSLSAVGDRVITITTRAGOSISSYLNWYQQRGKAPKLLIYAASLSQGVPSRF 62
QY 61 SGSSGGEFTLTITINLQFEDPASYYCOOSYTYLTYFGSGTKLEIKR 106
DB 63 SGSSGSDPTLITISLSLOPEDPATYTCQGSYSTL-TFGGDTNVEIKR 107
RESULT 3
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE IG kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC
DR EMBL, X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
DR PIR, A01883; KIH0WK.
DR HSSP, P01607; 1BMW.
DR SMR, P04431; 23-129.
DR Ensembl, ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006935; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.

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DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT REGION 23 45 /FTid=PRO_0000015170.
FT REGION 46 56 Framework-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Complementarity-determining-3.
FT REGION 111 119 Framework-3.
FT REGION 120 129 Complementarity-determining-4.
FT DISULFID 45 110 Framework-4.
FT NON TER 129 By similarity.
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 6.4e-40;
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDVVTITTCRAQGISITYLWYQOKPGKAPKLLIWSASNLQSGVTSRF 84
61 SSGSGCTEFTLTISNLQFEDFASVYCCQGSYTLTYFGSGTKLEIK 105
85 SSGSGCTDFTLTISLQPEDSATYCCQGSYSTLTITFGGTRLEIK 129

RESULT 4
KVLE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig kappa chain V-I region DEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstien C.P., Deveron B.V.;
RT "The amino acid sequence of a human kappa light chain.",
RL Biochem. J. 123:945-958(1971).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
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CC -----
CC PIR; A01865; KIHWD.
DR HSSP; P01607; IBMW.
DR SMR; P01597; 4-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006855; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
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FT CHAIN 1 >108 Ig kappa chain V-I region DEB.
FT REGION 1 23 /FTid=PRO_0000059741.
FT REGION 24 34 Framework-1.
FT REGION 35 49 Complementarity-determining-1.
FT REGION 50 56 Framework-2.
FT REGION 57 88 Complementarity-determining-2.
FT REGION 89 97 Framework-3.
FT REGION 98 98 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108.
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.4e-39;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 3 ZMTQSPSSLSASVGDVVTITTCRAQGSVNYKILWYQOKPGKAPKLLIWSASNLQSGVPSRF 62
61 SSGSGCTEFTLTISNLQFEDFASVYCCQGSYTLTYFGSGTKLEIK 106
63 SSGSGCTDFTLTISGLPEDFATYCCQGSYTLTYFGGTRLEIK 108

RESULT 5
Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.",
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
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CC -----
CC EMBL; AF035033; AAD56269.1; -; mRNA.
DR HSSP; P01607; IBMW.
DR Q9UL81; 1-107.
DR LinkHub; Q9UL81; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1 1.
FT NON TER 107 107.
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 82.0%; Score 448.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.6e-39;
Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVVTITTCRAQGISITYLWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
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Db      3 QMTQSPSSLSASVGDVYITTCRASQGISINYNWYQKPGKAPKALLIYAASSLSQGVPSRF 62
QY      61 SSGSGGTFFLTITSLNQFEDFASYYCQGSYTLTYFGSGTKLEIKR 106
Db      63 SSGSGGTDFLTITSLQAPDFATYYCQGSYSL-TFSPGTVKVDIR 107

RESULT 6
KV1H_HUMAN STANDARD; PRT; 108 AA.
ID      KV1H_HUMAN
AC      P01600;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      07-MAR-2006, entry version 44.
DE      Ig kappa chain V-I region Hau.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RX      MEDLINE=71032830; PubMed=4097974;
RA      Watanabe S., Hilschmann N.;
RT      "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT      chain of subgroup I (Bence-Jones protein Hau): subdivision within
RT      subgroups."
RL      Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC      -1- MISCELLANEOUS: This C region of this chain has the INV (3) marker.
CC      -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
DR      PIR; A01868; KIHUHU.
DR      PDB; 1F6U; X-ray; L=1-89.
DR      GO; GO:0005576; C:extracellular region; NMS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      InterPro; IPR013106; V-set.
DR      Pfam; PF07686; V-set; 1.
DR      SMART; SM00409; Ig; 1.
DR      SMART; SM00406; Ig; 1.
DR      PROSITE; PSS0835; IG LIKE; 1.
DR      3D-structure; Bence-Jones protein; Direct protein sequencing;
KW      Immunoglobulin domain; Immunoglobulin V region.
FT      CHAIN 1
FT      REGION 1 23 Framework-1.
FT      REGION 24 34 Complementarity-determining-1.
FT      REGION 35 49 Framework-2.
FT      REGION 50 56 Complementarity-determining-2.
FT      REGION 57 88 Framework-3.
FT      REGION 89 97 Framework-4.
FT      REGION 98 107 Complementarity-determining-3.
FT      DISULFID 23 88 Framework-4.
FT      NON_TER 108 108 By similarity.
FT      STRAND 4 7
FT      STRAND 9 12
FT      TURN 15 16
FT      STRAND 19 27
FT      TURN 30 31
FT      STRAND 33 38
FT      TURN 40 41
FT      STRAND 45 49
FT      TURN 50 52
FT      STRAND 53 54
FT      TURN 56 57
FT      TURN 60 61
FT      STRAND 62 67

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FT      TURN 68 69
FT      STRAND 70 75
FT      STRAND 77 77
FT      HELIX 80 82
FT      STRAND 84 90
FT      STRAND 92 95
FT      STRAND 98 98
FT      STRAND 102 105
SQ      SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 2.6e-38;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDVYITTCRASQGISINYNWYQKPGKAPKALLIYAASSLSQGVPSRF 60
Db      3 QMTQSPSSLSASVGDVYITTCRASQGISINYNWYQKPGKAPKALLIYAASSLSQGVPSRF 62
QY      61 SSGSGGTFFLTITSLNQFEDFASYYCQGSYTLTYFGSGTKLEIKR 106
Db      63 SSGSGGTDFLTITSLQAPDFATYYCQGSYSL-TFSPGTVKVDIR 108

RESULT 7
Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
ID      Q6GMX8_HUMAN
AC      Q6GMX8;
DT      19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT      19-JUL-2004, sequence version 1.
DT      07-FEB-2006, entry version 17.
DE      IGKC protein.
DE      Name=IGKC;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA      Datchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Heaton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA      Schnerch A., Schein J.B., Jones S.J.M., Maira M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Primary B-Cells;
RG      NIH MGC Project;
RL      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; BC073764; AAH73764.1; -; mRNA.
DR      SMR; Q6GMX8; 24-235.
DR      Ensembl; ENSG00000163245; Homo sapiens.

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DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; Cl-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGcl; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG-LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8B1AB6559EFC9 CRC64;

Query Match 79.2%; Score 433; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 1,7e-37;
Matches 82; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSIITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITCRASQGISSLWYQQKPGKAPKLLIYAASSLQGVPSRF 84

QY 61 SSGSGGTFTLTISNLOFEDFASYCQOSTYTLTYFGSGTKLEIKR 106
DB 85 SSGSGGTFTLTISLQPEDFATYCCQASHSPFTFGPGTKVDIKR 130

RESULT 8
Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 17.
ID IGKC protein.
GN IGKC protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC NIH MGC Project;
RG Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC073791; AAH73791.1; -; mRNA.
DR SMR: Q6GMW1; 24-236.
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; Cl-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGcl; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG-LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087APAC37 CRC64;

Query Match 78.8%; Score 431; DB 2; Length 236;
Best Local Similarity 79.2%; Pred. No. 2,8e-37;
Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQSIITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITCRASQGISLWYQQKPGKAPKLLIYAASSLQGVPSRF 84

QY 61 SSGSGGTFTLTISNLOFEDFASYCQOSTYTLTYFGSGTKLEIKR 106
DB 85 SSGSGGTFTLTISLQPEDFATYCCQASHSPFTFGPGTKVDIKR 130

RESULT 9
Q6GMX0_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 16.
ID Hypothetical protein.
GN Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC Strausberg R.;
RG Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; BC073775; AAH73775.1; -; mRNA.
DR      SMR; Q6GMX0; 23-236.
DR      Ensembl; ENSG00000163245; Homo sapiens.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG-V.
DR      InterPro; IPR013106; V-set.
DR      Pfam; PF07654; Cl-set; 1.
DR      SMART; SM00409; IG; 1.
DR      SMART; SM00407; IGcl; 1.
DR      SMART; SM00406; IG; 1.
DR      PROSITE; PS50835; IG-LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR      Hypothetical protein.
KW      SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match      78.6%; Score 430; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 3,6e-37;
Matches 82; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDRTVITTCRARGISITLYLWYQOKPKAPKLILWASNSLQGVPSRF 60
DB      25 QMTQSPSSLSASVGDRTVITTCRARGISINNTLYLWYQOKPKAPKLILWASNSLQGVPSRF 84
QY      61 SSGSGSTFEFTLTISLQFEDPASVYCOQSYTTLTYTSGSKLEIKR 106
DB      85 SSGSGSTFEFTLTISLRPDDPATVYCOQSYNIPLEFGGTVNVEIKR 130

RESULT 10
Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC      Q6PIH7;
DT      05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT      07-FEB-2006, entry version 17.
DE      IGKC protein.
GN      Name=IGKC;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Strausberg R.L., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA      Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Piatte C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whitting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```

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RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Lung;
RG      NIH MGC Project;
RL      Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
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CC      -----
DR      EMBL; BC034141; AAH34141.1; -; mRNA.
DR      SMR; P01607; 1A2.
DR      HSP; Q6PIH7; 23-236.
DR      Ensembl; ENSG00000163245; Homo sapiens.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003597; IG-cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG-V.
DR      InterPro; IPR013106; V-set.
DR      Pfam; PF07654; Cl-set; 1.
DR      SMART; SM00409; IG; 1.
DR      SMART; SM00407; IGcl; 1.
DR      SMART; SM00406; IG; 1.
DR      PROSITE; PS50835; IG-LIKE; 2.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR      SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match      78.2%; Score 428; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 5,9e-37;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDRTVITTCRARGISITLYLWYQOKPKAPKLILWASNSLQGVPSRF 60
DB      25 QLTQSPSSLSASVGDRTVITTCRARGISISLYLWYQOKPKAPKLILWASNSLQGVPSRF 84
QY      61 SSGSGSTFEFTLTISLQFEDPASVYCOQSYTTLTYTSGSKLEIKR 106
DB      85 SSGSGSTFEFTLTISLQFEDPATVYCOQLNSPPTFGGTVNVEIKR 130

RESULT 11
KV1N_HUMAN STANDARD; PRT; 108 AA.
ID      KV1N_HUMAN
AC      P01606;
DT      21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT      21-JUL-1986, sequence version 1.
DT      07-MAR-2006, entry version 39.
DE      Ig kappa chain V-I region EU.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RC      MEDLINE=70201507; PubMed=5447531;
RA      Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT      "Macroglobulin structure: variable sequence of light and heavy
RT      chains."
RL      Science 169:56-59(1970).
CC      -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC      -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC      macroglobulin.
CC      -----
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CC      -----
DR      PIR; A01872; K1HUOU.
DR      HSP; P01607; 1BWW.
DR      LinkHub; P01606; -.
DR      GO; GO:0005576; C:extracellular region; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.

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DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
DR Direct protein sequencing; Immunoglobulin domain;  
KM Immunoglobulin V region.  
PT CHAIN 1 >108  
FT REGION 1 23 Ig kappa chain V-I region OU.  
FT REGION 24 34 /FTID=PRO\_0000059748.  
FT REGION 35 49 Complementarity-determining-1.  
FT REGION 50 56 Framework-2.  
FT REGION 57 88 Complementarity-determining-2.  
FT REGION 89 97 Framework-3.  
FT REGION 98 107 Complementarity-determining-3.  
FT REGION 108 108 Framework-4.  
FT DISULFID 23 88 By similarity.  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11779 MW; 8283D4A24105827E CRC64;  
  
Query Match 77.5%; Score 424; DB 1; Length 108;  
Best Local Similarity 68.3%; Pred. No. 6.3e-37;  
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 ELTQSPSSLSASVGDVTTICRARQSIITYLWYQKRGKAPKLLIYMSASNLQSGVPSRF 60  
Db 3 QMTZSPSSLSASVGBRYTTICRASZTISYLBWYZZKPGKAPLLIYAAIBLHSGVPSRF 62  
  
QY 61 GSGSGSTEFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
Db 63 GSGSGSTBFTLTISLZPZBFATYYCZSYSPFTTGZTRLKIKR 108  
  
RESULT 12  
ID 072473\_HUMAN PRELIMINARY; PRT; 234 AA.  
AC 072473;  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12479392; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marutisa K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stropstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Tohiyuki S., Caminci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Heaton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Maan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein U.E., Jones S.U.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RG NIH MGC Project;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; BC056256; AAH56256.1; -; mRNA.  
DR HSSP; P01834; 1HE2.  
DR SMR; Q72473; 22-234.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; Ig; 1.  
DR SMART; SM00407; Igcl; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.  
DR SEQUENCE 234 AA; 35674 MW; 1A2C259BAB51BC0F CRC64;  
  
Query Match 77.3%; Score 423; DB 2; Length 234;  
Best Local Similarity 78.1%; Pred. No. 2e-36;  
Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
  
QY 2 LTQSPSSLSASVGDVTTICRARQSIITYLWYQKRGKAPKLLIYMSASNLQSGVPSRF 61  
Db 24 MTQSPSSFSASIDRYTTICRASQSIGSYLWYQKRGKAPQLLIYAAIBLHSGVPSRF 83  
  
QY 62 GSGSGSTEFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
Db 84 GSASGTDFTLTISLCLQSEDFATYYCQQYTYPTFGGTVEIKR 128  
  
RESULT 13  
ID KV1B\_HUMAN STANDARD; PRT; 108 AA.  
AC KV1B\_HUMAN  
AC P01554;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 21-JUL-1986, sequence version 1.  
DT 07-MAR-2006, entry version 46.  
DE Ig kappa chain V-I region AU.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=72189444; PubMed=5028201;  
RA Schiechl H., Hilschmann N.,  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
RT protein Au).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=77022433; PubMed=1234024;  
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
RA Schwager P., Steigemann W., Schramm H.J.,  
RT "The structure determination of the variable portion of the Bence-  
RT Jones protein Au";  
RL Biophys. Struct. Mech. 1:139-146(1975).  
CC -; MISCELLANEOUS: The structure of the V region was determined by  
CC molecular replacement methods using the known structure of the V  
CC region of the kappa chain REI.

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CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC -----
DR PIR; A91653; KIHUUV.
DR PDB; 1BW5; X-ray; A/B/C=1-108.
DR PDB; 1JY5; X-ray; A=1-107.
DR Ensemble; ENSG00000173782; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
KW CHAIN 1 >108
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
FT STRAND 4 5
FT STRAND 7 7
FT STRAND 9 13
FT TURN 15 16
FT STRAND 19 27
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FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
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FT STRAND 80 82
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FT STRAND 92 95
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 76.4%; Pred. No. 4.4e-36;
Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSIASVDRVYITTCAROSISTYLNWYQOKRGKAPKLLINSASNLQGVPSRF 60
DB 3 QMTQSPSSLSASVDGVYITTCQASQDSDYLNWYQOKRGKAPKLLITYDASNLQGVPSRF 62
QY 61 SGSGSGTEFTLLINLQFEDPASYYCQGSYTLTYFGSGTKLEIKR 106
DB 63 SGSGSGAHFTTISLSIQPEDIAITYCCQYDYLPTWFGGTVEIKR 108

RESULT 14
KV10_HUMAN

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ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-UTL-1986, sequence version 1.
DT 07-MAR-2006, entry version 51.
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Latman E.B., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR PIR; A91653; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BW5; X-ray; A/B=1-107.
DR PDB; 1RET; X-ray; A/B=1-107.
DR LinkHub; P01607; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
KW CHAIN 1 >108
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88
FT NON_TER 108 108
FT STRAND 4 7
FT STRAND 9 13
FT TURN 15 16
FT STRAND 19 27
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 42 42

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FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 77
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 92 95
FT STRAND 97 98
FT STRAND 102 106
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCEZA CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 4,4e-36;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

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Db 3 QMTQSPSSLSASVGDRTVITTCRAQSISQDILKILNMYQOTPGKAPKLLIWEASNLQAGVPSRF 62
QY 61 SSGSGSGTEFTLTITSLNQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
Db 63 SSGSGSGTDYFTLTITSLQPEDVATYYCCQYQSLPYTFGQGTQLQITR 108

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AC Q9UL70;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Diamond B.
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA Manheimer-Lory A., Katz J.B., Pfallinger M., Ghosein C., Smith A.,
RA Diamond B.
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idioType.";
RL J. Exp. Med. 174:1639-1652(1991).
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CC
EMBL: AF035044; AAD56280.1; -, mRNA.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.

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FT NON TER 1 1
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Query Match 75.7%; Score 414; DB 2; Length 108;
Best Local Similarity 77.4%; Pred. No. 7.2e-36;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

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QY 61 SSGSGSGTEFTLTITSLNQFEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
Db 63 SSGSGSGTDYFTLTITSLQPEDVATYYCCQYNSAPRTFGPGTKLEIKR 108

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Search completed: August 30, 2006, 00:35:14  
Job time : 58.8182 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 14.4545 Seconds  
(without alignments)  
641.891 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547  
Sequence: 1 ELTQSPSSASAVGDRVIT.....QQSYTLTYFGSGTKLKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/prodata/2/1aa/5 COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/1aa/6 COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/1aa/7 COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/1aa/H COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/1aa/PCTUS COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/1aa/RE COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	88.5	107	1 US-08-276-852-104	Sequence 104, App
2	484	88.5	107	1 US-08-899-575-104	Sequence 104, App
3	484	88.5	107	1 US-08-899-575-104	Sequence 104, App
4	484	88.5	107	5 PCT-US95-08743-104	Sequence 104, App
5	483	88.3	107	2 US-09-240-274-33	Sequence 33, App1
6	480	87.8	107	2 US-09-848-798-33	Sequence 33, App1
7	480	87.8	107	2 US-09-240-274-156	Sequence 156, App
8	480	87.8	107	2 US-09-848-798-156	Sequence 156, App
9	476	87.0	107	1 US-08-276-852-105	Sequence 105, App
10	476	87.0	107	1 US-08-899-575-105	Sequence 105, App
11	476	87.0	107	1 US-08-899-575-105	Sequence 105, App
12	476	87.0	107	5 PCT-US95-08743-105	Sequence 105, App
13	475	86.8	107	2 US-09-240-274-175	Sequence 175, App
14	475	86.8	107	2 US-09-240-274-176	Sequence 176, App
15	475	86.8	107	2 US-09-848-798-175	Sequence 175, App
16	475	86.8	107	2 US-09-848-798-176	Sequence 176, App
17	474	86.7	107	2 US-09-240-274-179	Sequence 179, App
18	474	86.7	107	2 US-09-848-798-179	Sequence 179, App
19	473.5	86.6	108	2 US-09-240-274-32	Sequence 32, App1
20	473.5	86.6	108	2 US-09-240-274-43	Sequence 43, App1
21	473.5	86.6	108	2 US-09-848-798-32	Sequence 32, App1
22	473.5	86.6	108	2 US-09-848-798-43	Sequence 43, App1
23	473	86.5	107	2 US-09-240-274-37	Sequence 37, App1
24	473	86.5	107	2 US-09-848-798-37	Sequence 37, App1
25	472.5	86.4	108	2 US-09-240-274-167	Sequence 167, App
26	472.5	86.4	108	2 US-09-848-798-167	Sequence 167, App

27	472	86.3	107	2 US-09-240-274-38	Sequence 38, App1
28	472	86.3	107	2 US-09-240-274-39	Sequence 39, App1
29	472	86.3	107	2 US-09-240-274-162	Sequence 162, App
30	472	86.3	107	2 US-09-848-798-38	Sequence 38, App1
31	472	86.3	107	2 US-09-848-798-39	Sequence 39, App1
32	472	86.3	107	2 US-09-848-798-162	Sequence 162, App
33	471	86.1	107	2 US-09-240-274-158	Sequence 158, App
34	471	86.1	107	2 US-09-848-798-158	Sequence 158, App
35	469	85.7	107	2 US-09-240-274-44	Sequence 44, App1
36	469	85.7	107	2 US-09-848-798-44	Sequence 44, App1
37	468	85.6	108	1 US-08-379-057-29	Sequence 29, App1
38	467	85.4	240	2 US-09-192-854-2	Sequence 2, App1
39	467	85.4	240	2 US-09-511-939-2	Sequence 2, App1
40	464.5	84.9	108	2 US-09-240-274-163	Sequence 163, App
41	464.5	84.9	108	2 US-09-848-798-163	Sequence 163, App
42	463	84.6	104	1 US-08-276-852-106	Sequence 106, App
43	463	84.6	104	1 US-08-899-575-106	Sequence 106, App
44	463	84.6	104	1 US-08-899-575-106	Sequence 106, App
45	463	84.6	104	5 PCT-US95-08743-106	Sequence 106, App

## ALIGNMENTS

RESULT 1  
US-08-276-852-104  
Sequence 104, Application US/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Filting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-276-852-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 2.2e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKKLIWASNLQSGVPSRF 60

Qy 61 SSGSGGTFTLTISNLOPEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
Db 61 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFQGTKEIKR 106

RESULT 2  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

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Best Local Similarity 88.7%; Pred. No. 2.2e-36;  
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Db 61 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFQGTKEIKR 106

RESULT 3  
US-08-899-575-104  
; Sequence 104, Application US/08899575  
; Patent No. 5804440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lerner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRI452P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 104:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;  
Best Local Similarity 88.7%; Pred. No. 2.2e-36;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKKLIWASNLQSGVPSRF 60  
Db 1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQKPKKLIWASNLQSGVPSRF 60

Qy 61 SSGSGGTFTLTISNLOPEDFASYYCOQSYTTLTYFGSGTKLEIKR 106  
Db 61 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFQGTKEIKR 106

RESULT 4  
PCT-US95-08743-104

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; Sequence 104, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
PCT-US95-08743-104

Query Match      88.5%; Score 484; DB 5; Length 107;
Best Local Similarity 88.7%; Pred. No. 2.2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
QY 61 SSGSGSTDEFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
DB 61 SSGSGSTDEFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEO ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match      88.3%; Score 483; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.7e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

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QY 61 SSGSGSTDEFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
DB 61 SSGSGSTDEFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
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DB 62 SSGSGSTDEFTLTISNLOPEDFASYCQOSYSTLTMTFGGCKVEIKR 107

RESULT 6
US-09-848-798-33
; Sequence 33, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; EARLIER FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEO ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match      88.3%; Score 483; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.7e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 61
QY 61 SSGSGSTDEFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106
DB 62 SSGSGSTDEFTLTISNLOPEDFASYCQOSYSTLTMTFGGCKVEIKR 107

RESULT 7
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEO ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      87.8%; Score 480; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 5e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRAROSISTYLMWYQKPKAPKLLIWSASNLQSGVPSRF 61
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QY 61 SGGSGTEFTLTISNLQFEDPASYYCCQSYTTLTFRSGTKLEIKR 106  
62 SGGSGGTDFTLTISSLQPDPAATYYCCQSYSTPTFTGGTKLEIKR 107  
Db

RESULT 8  
TTC-00-94

US-09-848-798-156  
 , Sequence 156, Application US/09848798  
 , Patent No. 6858719  
 , GENERAL INFORMATION:  
 , APPLICANT: Siegel, Donald L.  
 , TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS  
 , TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 , FILE REFERENCE: 09596-4202  
 , CURRENT APPLICATION NUMBER: US/09/848,798  
 , PRIOR FILING DATE: 2001-05-04  
 , PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
 , PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
 , PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
 , PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
 , NUMBER OF SEQ ID NOS: 224  
 , SOFTWARE: PatentIn Ver. 2.0  
 , SEQ ID NO 156  
 , LENGTH: 107  
 , TYPE: PRT  
 , ORGANISM: Homo sapiens  
 , FEATURE:  
 , OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
 , US-09-848-798-156

Query Match	87.8%	Score 480;	DB 2;	Length 107;
Best Local Similarity	87.7%	Pred. No. 5e-36;		
Matches 93;	Conservative 9;	Mismatches 4;	Indels 0;	Gaps 0;

QY ELTQSPSLSLASVQDRVLTITTCRAQSTISLYTNWYQQRGKAPKLLIMASNLQSGVPSRR 6  
Db ELTQSPSLSLASVQDRVLTITTCRAQSTISLYTNWYQQRGKAPKLLIMASNLQSGVPSRR 6  
QY 2 ELTQSPSLSLASVQDRVLTITTCRAQSTISLYTNWYQQRGKAPKLLIMASNLQSGVPSRR 6  
QY 61 SGSSGSEFTLTISNLQDPASYYCOOSYTLTLTBSSGKLEIKR 106  
Db 62 SGSSGSDITLTISLSLPQPAITYCOOSSTPITPQGRKLEIKR 107

## RESULT 5

US-08-276-852-105  
Sequence 105, Application us/08276852  
Patent No. 5652138  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbas, Carlos F  
APPLICANT: Lerner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSER: Patent Counsel  
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/276,852  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148

Query Match	87.0%;	Score 476;	DB 1;	Length 107;
Best Local Similarity	87.7%;	Pred. No. 1.1e-35;		
Matches 93;	Conservative 8;	Mismatches 5;	Indels 0;	Gaps 0;

QY	1	ELTQSPSSLASVGDRTITICRAPOSISTYLNNYQKPGCAPRLTIYASSTLQSGVPSRF	60
Db	1	ELTQSPSSLASVGDRTITICRAQSISSTLNNYQKPGCAPRLTIYASSTLQSGVPSRF	60
QY	61	SGSSSGTEFTLLTSLNLFQDFPASYCQOSTTLYTGSGTKLEIKR	106
Db	61	SGSSSGTDFLTLLTSLNLFQDFPASYCQOSTTLYTGSGTKLEIKR	106

## RESULT 10

US-08-899-575-105  
; Sequence 105, Application US/08899575  
; Patent No. 5770440  
; GENERAL INFORMATION:  
; APPLICANT: Burton, Dennis R  
; APPLICANT: Barbas, Carlos F  
; APPLICANT: Lemner, Richard A  
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
; NUMBER OF SEQUENCES: 170  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,  
; STREET: Mail Drop TPC8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/899,575  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/276,852  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: US 08/178,302  
; FILING DATE: 30-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/954,148  
; FILING DATE: 30-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas



REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.1e-35;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRARSISITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60  
QY 61 SSGSGGTFTLTISLQPEDFATYVCCQSYSTPTGTGQTKLEIKR 106  
DB 61 SSGSGGTFTLTISLQPEDFATYVCCQSYSTPTGTGQTKLEIKR 106

RESULT 11  
US-08-899-575-105  
Sequence 105, Application US/08899575  
Patent No. 5804440  
GENERAL INFORMATION:  
APPLICANT: Burton, Dennis R  
APPLICANT: Barbae, Carlos F  
APPLICANT: Leiner, Richard A  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,  
STREET: Mail Drop TPC8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899,575  
FILING DATE: 24-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: US 08/178,302  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/954,148  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRI452P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.1e-35;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRARSISITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60  
QY 61 SSGSGGTFTLTISLQPEDFATYVCCQSYSTPTGTGQTKLEIKR 106  
DB 61 SSGSGGTFTLTISLQPEDFATYVCCQSYSTPTGTGQTKLEIKR 106

RESULT 12  
PCT-US95-08743-105  
Sequence 105, Application PC/TUS9508743  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08743  
FILING DATE: 11-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/276,852  
FILING DATE: 18-JUL-1994  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08743-105

Query Match 87.0%; Score 476; DB 5; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.1e-35;  
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDRTVITTCRARSISITYLNMVYQKPGKAPKLLIWSASNLQGVPSRF 60  
QY 61 SSGSGGTFTLTISLQPEDFATYVCCQSYSTPTGTGQTKLEIKR 106  
DB 61 SSGSGGTFTLTISLQPEDFATYVCCQSYSTPTGTGQTKLEIKR 106

RESULT 13  
US-09-240-274-175  
Sequence 175, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/09/240,274  
FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11

```

; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

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Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.4e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIYAASSLQSGVPSRF 61

```

```

QY 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTTLYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 62 SGSGSGTDFLTITISLQPEDFATYCCOOSYSTPWTFGGTVKEIKR 107

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```

RESULT 14
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

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```

Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.4e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIYAASSLQSGVPSRF 61

```

```

QY 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTTLYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 62 SGSGSGTDFLTITISLQPEDFATYCCOOSYSTPWTFGGTVKEIKR 107

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RESULT 15
US-09-848-798-175
; Sequence 175, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274

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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

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```

Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.4e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKPGKAPKLLIYAASSLQSGVPSRF 61

```

```

QY 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTTLYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 62 SGSGSGTDFLTITISLQPEDFATYCCOOSYSTPWTFGGTVKEIKR 107

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Search completed: August 30, 2006, 00:37:08
Job time : 15.4545 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 60.7091 Seconds  
(without alignments)  
808.788 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547  
Sequence: 1 ELTQSPSSISASVGDVITIT.....QOSYTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/Pcdata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/Pcdata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/Pcdata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/Pcdata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/Pcdata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/Pcdata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	547	100.0	106	4	US-10-027-725A-11	Sequence 11, App1
2	484	88.5	107	4	US-10-016-986-104	Sequence 104, App
3	483	88.3	107	3	US-09-848-798-33	Sequence 33, App1
4	483	88.3	107	6	US-11-064-174-33	Sequence 33, App1
5	480	87.8	107	3	US-09-848-798-156	Sequence 156, App
6	480	87.8	107	6	US-11-064-174-156	Sequence 156, App
7	476	87.0	107	4	US-10-016-986-105	Sequence 105, App
8	475	86.8	107	3	US-09-848-798-175	Sequence 175, App
9	475	86.8	107	6	US-11-064-174-175	Sequence 175, App
10	475	86.8	107	6	US-11-064-174-176	Sequence 176, App
11	475	86.8	107	3	US-09-848-798-179	Sequence 179, App
12	474	86.7	107	6	US-11-064-174-179	Sequence 179, App
13	474	86.7	107	3	US-09-848-798-32	Sequence 32, App1
14	473.5	86.6	108	3	US-09-848-798-43	Sequence 43, App1
15	473.5	86.6	108	6	US-11-064-174-32	Sequence 32, App1
16	473.5	86.6	108	6	US-11-064-174-43	Sequence 43, App1
17	473.5	86.6	107	3	US-09-848-798-37	Sequence 37, App1
18	473	86.5	107	6	US-11-064-174-37	Sequence 37, App1
19	473	86.5	109	6	US-11-127-932-16	Sequence 16, App1
20	473	86.5	109	6	US-11-127-932-17	Sequence 17, App1
21	473	86.5	109	6	US-11-127-932-20	Sequence 20, App1
22	473	86.5	109	6	US-11-127-903-16	Sequence 16, App1
23	473	86.5	109	6	US-11-127-903-17	Sequence 17, App1
24	473	86.5	109	6	US-11-127-903-20	Sequence 20, App1
25	473	86.5	109	6	US-11-127-903-32	Sequence 32, App1
26	473	86.5	111	4	US-10-203-754A-57	Sequence 57, App1
27	472.5	86.4	108	3	US-09-848-798-167	Sequence 167, App

28	472.5	86.4	108	6	US-11-064-174-167	Sequence 167, App
29	472	86.3	107	3	US-09-848-798-38	Sequence 38, App1
30	472	86.3	107	3	US-09-848-798-39	Sequence 39, App1
31	472	86.3	107	3	US-09-848-798-162	Sequence 162, App
32	472	86.3	107	6	US-11-064-174-38	Sequence 38, App1
33	472	86.3	107	6	US-11-064-174-39	Sequence 39, App1
34	472	86.3	107	6	US-11-064-174-162	Sequence 162, App
35	472	86.3	116	5	US-10-783-311-198	Sequence 198, App
36	471	86.1	107	3	US-09-848-798-158	Sequence 158, App
37	471	86.1	107	6	US-11-064-174-158	Sequence 158, App
38	470	85.9	157	6	US-11-131-648-27	Sequence 27, App1
39	470	85.9	157	6	US-11-131-648-63	Sequence 63, App1
40	469	85.7	107	3	US-09-848-798-44	Sequence 44, App1
41	469	85.7	107	6	US-11-064-174-44	Sequence 44, App1
42	468	85.6	108	5	US-10-726-332-209	Sequence 209, App
43	468	85.6	111	4	US-10-203-754A-56	Sequence 56, App1
44	467	85.4	108	4	US-10-409-814A-4	Sequence 4, App1
45	467	85.4	108	5	US-10-477-830-90	Sequence 90, App1

#### ALIGNMENTS

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RESULT 1
US-10-027-725A-11
; Sequence 11, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; CURRENT FILING DATE: 2000-12-29
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-11

Query Match      100.0%; Score 547; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.2e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELTQSPSSISASVGDVITTCRARQGISITLWNYQKPGKAPKLLIWSASNLQGVPSRF 60
      |||
DB      1 ELTQSPSSISASVGDVITTCRARQGISITLWNYQKPGKAPKLLIWSASNLQGVPSRF 60
      |||

QY      61 SGSGSGTEFTLTNSIQFEDFASVYCOOSYTLTYTSGSGTKLEIKR 106
      |||
DB      61 SGSGSGTEFTLTNSIQFEDFASVYCOOSYTLTYTSGSGTKLEIKR 106
      |||

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR FILING DATE: 1998-09-08
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
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;; PRIOR APPLICATION NUMBER: US 08/276,852  
;; PRIOR FILING DATE: 1994-07-18  
;; PRIOR APPLICATION NUMBER: US 08/178,302  
;; PRIOR FILING DATE: 1994-01-06  
;; PRIOR APPLICATION NUMBER: PCT/US93/09328  
;; PRIOR FILING DATE: 1993-09-30  
;; PRIOR APPLICATION NUMBER: US 07/954,148  
;; PRIOR FILING DATE: 1992-09-30  
;; NUMBER OF SEQ ID NOS: 176  
;; SOFTWARE: PatSeq for Windows Version 4.0  
;; SEQ ID NO 104  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthesized  
US-10-016-986-104

Query Match 88.5%; Score 484; DB 4; Length 107;  
Best Local Similarity 88.7%; Pred. No. 1.3e-34;  
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIYAASLSQGVPSRF 60  
QY 61 SSGSGGTFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
DB 61 SSGSGGTFTLTISNLOPEDFATYCCQOSYSTPTTFGQTKLEIKR 106

## RESULT 3

US-09-848-798-33  
;; Sequence 33, Application US/09848798  
;; Publication No. US20030040605A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Siegel, Donald L.  
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
;; FILE REFERENCE: 09596-42U2  
;; CURRENT APPLICATION NUMBER: US/09/848,798  
;; CURRENT FILING DATE: 2001-05-04  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 33  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: anti-Rh(D) chain 102  
US-09-848-798-33

Query Match 88.3%; Score 483; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.6e-34;  
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIYAASLSQGVPSRF 61  
QY 61 SSGSGGTFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
DB 62 SSGSGGTFTLTISNLOPEDFATYCCQOSYSTPTTFGQTKLEIKR 107

RESULT 4  
US-11-064-174-33  
;; Sequence 33, Application US/11064174  
;; Publication No. US20050282252A1

;; GENERAL INFORMATION:  
;; APPLICANT: Siegel, Donald L.  
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
;; FILE REFERENCE: 09596-42U2  
;; CURRENT APPLICATION NUMBER: US/11/064,174  
;; CURRENT FILING DATE: 2005-02-22  
;; PRIOR APPLICATION NUMBER: US/09/240,274  
;; PRIOR FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: 60/081,380  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 33  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: anti-Rh(D) chain 102  
US-11-064-174-33

Query Match 88.3%; Score 483; DB 6; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1.6e-34;  
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIYAASLSQGVPSRF 61  
QY 61 SSGSGGTFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
DB 62 SSGSGGTFTLTISNLOPEDFATYCCQOSYSTPTTFGQTKLEIKR 107

## RESULT 5

US-09-848-798-156  
;; Sequence 156, Application US/09848798  
;; Publication No. US20030040605A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Siegel, Donald L.  
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
;; FILE REFERENCE: 09596-42U2  
;; CURRENT APPLICATION NUMBER: US/09/848,798  
;; CURRENT FILING DATE: 2001-05-04  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 156  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
US-09-848-798-156

Query Match 87.8%; Score 480; DB 3; Length 107;  
Best Local Similarity 87.7%; Pred. No. 2.9e-34;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPGKAPKLLIYAASLSQGVPSRF 61  
QY 61 SSGSGGTFTLTISNLOPEDFASYCQOSYTTLYTFGSGTKLEIKR 106  
DB 62 SSGSGGTFTLTISNLOPEDFATYCCQOSYSTPTTFGQTKLEIKR 107

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RESULT 6
US-11-064-174-156
; Sequence 156, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-064-174-156

Query Match      87.8%; Score 480; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 2,9e-34;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARGISITLWYQKPKAKPLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRARGISITLWYQKPKAKPLIWSASNLQSGVPSRF 61
QY 61 SSGSGSTFTLTISNLFQEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGSTFTLTITSSLPEDFATYCCQSYSTPFTGGTKLEIKR 107

RESULT 7
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CONT1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match      87.0%; Score 476; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 6,5e-34;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARGISITLWYQKPKAKPLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDVVTITTCRARGISITLWYQKPKAKPLIWSASNLQSGVPSRF 60
QY 61 SSGSGSTFTLTISNLFQEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGSTFTLTITSSLPEDFATYCCQSYSTPFTGGTKLEIKR 106

RESULT 8
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 7,9e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARGISITLWYQKPKAKPLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITTCRARGISITLWYQKPKAKPLIWSASNLQSGVPSRF 61
QY 61 SSGSGSTFTLTISNLFQEDFASVYCCQSYTTLTYFGSGTKLEIKR 106
DB 62 SSGSGSTFTLTITSSLPEDFATYCCQSYSTPFTGGTKLEIKR 107

RESULT 9
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
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TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-09-848-798-176

Query Match 86.8%; Score 475; DB 3; Length 107;  
Best Local Similarity 85.8%; Pred. No. 7.9e-34;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFSGSKLEIKR 106  
DB 62 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPWTFGQTKVEIKR 107

## RESULT 10

US-11-064-174-175  
Sequence 175, Application US/11064174  
Publication No. US20050282252A1  
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/11/064,174  
CURRENT FILING DATE: 2005-02-22

PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 175  
LENGTH: 107

TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH49

US-11-064-174-175

Query Match 86.8%; Score 475; DB 6; Length 107;  
Best Local Similarity 85.8%; Pred. No. 7.9e-34;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFSGSKLEIKR 106  
DB 62 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPWTFGQTKVEIKR 107

## RESULT 11

US-11-064-174-176  
Sequence 176, Application US/11064174  
Publication No. US20050282252A1  
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/11/064,174  
CURRENT FILING DATE: 2005-02-22

PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/081,380

PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 176  
LENGTH: 107

TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-11-064-174-176

Query Match 86.8%; Score 475; DB 6; Length 107;  
Best Local Similarity 85.8%; Pred. No. 7.9e-34;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFSGSKLEIKR 106  
DB 62 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPWTFGQTKVEIKR 107

## RESULT 12

US-09-848-798-179  
Sequence 179, Application US/09848798  
Publication No. US20030040605A1  
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2

CURRENT APPLICATION NUMBER: US/09/848,798  
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 179  
LENGTH: 107

TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-179

Query Match 86.7%; Score 474; DB 3; Length 107;  
Best Local Similarity 85.8%; Pred. No. 9.6e-34;  
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDRTVITTCRARSISITLNMWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLOFEDFASYCOQSYTTLYTFSGSKLEIKR 106  
DB 62 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPWTFGQTKVEIKR 107

## RESULT 13

US-11-064-174-179  
Sequence 179, Application US/11064174  
Publication No. US20050282252A1  
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-42U2

Search completed: August 30, 2006, 00:50:37  
Job time : 61.7091 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 12.5273 Seconds  
(without alignments)  
578.960 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547  
Sequence: 1 ELTQSPSSIASVGDVRVIT.....QQSYTTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Published Applications AA.New:\*  
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2: /EMC\_Celerra\_SIDS3/ptocdata/2/pubpaa/US06\_NEW\_PUB pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	88.3	107	US-11-328-483-33	Sequence 33, App1
2	480	87.8	107	US-11-328-483-156	Sequence 156, App
3	475	86.8	107	US-11-328-483-175	Sequence 175, App
4	475	86.8	107	US-11-328-483-176	Sequence 176, App
5	474	86.7	107	US-11-328-483-179	Sequence 179, App
6	473.5	86.6	108	US-11-328-483-32	Sequence 32, App1
7	473.5	86.6	108	US-11-328-483-43	Sequence 43, App1
8	473	86.5	107	US-11-328-483-37	Sequence 37, App1
9	472.5	86.4	108	US-11-328-483-167	Sequence 167, App
10	472	86.3	107	US-11-328-483-38	Sequence 38, App1
11	472	86.3	107	US-11-328-483-39	Sequence 39, App1
12	472	86.3	107	US-11-328-483-162	Sequence 162, App
13	471	86.1	106	US-11-337-300-41	Sequence 41, App1
14	471	86.1	107	US-11-328-483-158	Sequence 158, App
15	471	86.1	107	US-11-337-300-47	Sequence 47, App1
16	471	86.1	244	US-11-317-786B-17	Sequence 17, App1
17	471	86.1	244	US-11-317-786B-19	Sequence 19, App1
18	471	86.1	245	US-11-337-300-51	Sequence 51, App1
19	471	86.1	245	US-11-337-300-53	Sequence 53, App1
20	471	86.1	245	US-11-337-300-59	Sequence 59, App1
21	471	86.1	245	US-11-337-300-63	Sequence 63, App1
22	471	86.1	247	US-11-337-300-57	Sequence 57, App1
23	471	86.1	247	US-11-337-300-96	Sequence 96, App1
24	471	86.1	248	US-11-337-300-61	Sequence 61, App1
25	471	86.1	249	US-11-337-300-49	Sequence 49, App1

26	471	86.1	249	7	US-11-337-300-67	Sequence 67, App1
27	471	86.1	249	7	US-11-337-300-69	Sequence 69, App1
28	471	86.1	249	7	US-11-337-300-90	Sequence 90, App1
29	471	86.1	249	7	US-11-337-300-92	Sequence 92, App1
30	469	85.7	217	7	US-11-328-483-44	Sequence 44, App1
31	466	85.2	214	7	US-11-337-300-129	Sequence 129, App
32	466	85.2	214	7	US-11-317-786B-13	Sequence 13, App1
33	465	85.0	240	7	US-11-317-786B-15	Sequence 15, App1
34	464.5	84.9	108	7	US-11-328-483-163	Sequence 163, App
35	463	84.6	107	7	US-11-375-221-103	Sequence 103, App
36	462	84.5	105	7	US-11-333-197-52	Sequence 52, App1
37	462	84.5	105	7	US-11-354-679-9	Sequence 9, App11
38	461	84.3	249	6	US-10-539-402-16	Sequence 16, App
39	459	83.9	107	7	US-11-328-483-168	Sequence 168, App
40	457	83.5	107	7	US-11-328-483-36	Sequence 36, App1
41	457	83.5	109	7	US-11-094-132-75	Sequence 75, App1
42	456.5	83.5	108	7	US-11-328-483-41	Sequence 41, App1
43	456	83.4	107	7	US-11-328-483-173	Sequence 173, App
44	455.5	83.3	105	6	US-10-981-300-24	Sequence 24, App1
45	454	83.0	107	7	US-11-328-483-40	Sequence 40, App1

#### ALIGNMENTS

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RESULT 1
US-11-328-483-33
; Sequence 33, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/328,483
; PRIOR APPLICATION NUMBER: 2006-01-09
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rn(D) chain 102
US-11-328-483-33

Query Match      88.3%; Score 483; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 7, 3e-38;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY      1 ELTQSPSSIASVGDVRVITTCAROSISTYLMWYQKPKAPKLILWASNLQSGVPSRF 60
Db      2 ELTQSPSSIASVGDVRVITTCAROSISTYLMWYQKPKAPKLILWASNLQSGVPSRF 61
QY      61 SSGSGTFTLTLSNCFEDFASYQOQSYTLTYFGSGTKLEIKR 106
Db      62 SSGSGTFTLTLSLQPFDFATYTCQOSYSTLWTFGSGTKLEIKR 107

RESULT 2
US-11-328-483-156
; Sequence 156, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
```

;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; FILE REFERENCE: 09596-4202  
;; CURRENT APPLICATION NUMBER: US/11/328,483  
;; PRIOR FILING DATE: 2006-01-09  
;; PRIOR APPLICATION NUMBER: US/11/064,174  
;; PRIOR FILING DATE: 2005-02-22  
;; PRIOR APPLICATION NUMBER: US/09/240,274  
;; PRIOR FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: 60/081,380  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 156  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH13  
US-11-328-483-156

Query Match 87.8%; Score 480; DB 7; Length 107;  
Best Local Similarity 87.7%; Pred. No. 1,4e-37;  
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLNWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTTCRAROSISSYLNWYQKRGKAPKLLIYAASSLQSGVPSRF 61  
QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOOSYTTLYTFSGSTKLEIKR 106  
DB 62 SSGSGGTEFTLTISNLOPEDFATYYCOOSYSTPTTFGGTKVEIKR 107

RESULT 3  
US-11-328-483-175

;; Sequence 175, Application US/11328483  
;; Publication No. US20060177440A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Siegel, Donald L.  
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; FILE REFERENCE: 09596-4202  
;; CURRENT APPLICATION NUMBER: US/11/328,483  
;; CURRENT FILING DATE: 2006-01-09  
;; PRIOR APPLICATION NUMBER: US/11/064,174  
;; PRIOR FILING DATE: 2005-02-22  
;; PRIOR APPLICATION NUMBER: US/09/240,274  
;; PRIOR FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: 60/081,380  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 175  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH49  
US-11-328-483-175

Query Match 86.8%; Score 475; DB 7; Length 107;  
Best Local Similarity 85.8%; Pred. No. 4e-37;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLNWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTTCRAROSISSYLNWYQKRGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOOSYTTLYTFSGSTKLEIKR 106  
DB 62 SSGSGGTEFTLTISNLOPEDFATYYCOOSYSTPTTFGGTKVEIKR 107

RESULT 4  
US-11-328-483-176

;; Sequence 176, Application US/11328483  
;; Publication No. US20060177440A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Siegel, Donald L.  
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; FILE REFERENCE: 09596-4202  
;; CURRENT APPLICATION NUMBER: US/11/328,483  
;; CURRENT FILING DATE: 2006-01-09  
;; PRIOR APPLICATION NUMBER: US/11/064,174  
;; PRIOR FILING DATE: 2005-02-22  
;; PRIOR APPLICATION NUMBER: US/09/240,274  
;; PRIOR FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: 60/081,380  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 176  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: anti-Rh(D) antibody clone SH50  
US-11-328-483-176

Query Match 86.8%; Score 475; DB 7; Length 107;  
Best Local Similarity 85.8%; Pred. No. 4e-37;  
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTTCRAROSISTYLNWYQKRGKAPKLLIWSASNLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTTCRAROSISSYLNWYQKRGKAPKLLIYAASSLQSGVPSRF 61  
QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOOSYTTLYTFSGSTKLEIKR 106  
DB 62 SSGSGGTEFTLTISNLOPEDFATYYCOOSYSTPTTFGGTKVEIKR 107

RESULT 5  
US-11-328-483-179

;; Sequence 179, Application US/11328483  
;; Publication No. US20060177440A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Siegel, Donald L.  
;; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
;; FILE REFERENCE: 09596-4202  
;; CURRENT APPLICATION NUMBER: US/11/328,483  
;; CURRENT FILING DATE: 2006-01-09  
;; PRIOR APPLICATION NUMBER: US/11/064,174  
;; PRIOR FILING DATE: 2005-02-22  
;; PRIOR APPLICATION NUMBER: US/09/240,274  
;; PRIOR FILING DATE: 1999-01-29  
;; PRIOR APPLICATION NUMBER: 60/081,380  
;; PRIOR FILING DATE: 1998-04-10  
;; PRIOR APPLICATION NUMBER: 60/028,550  
;; PRIOR FILING DATE: 1996-10-11  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 179  
;; LENGTH: 107  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:

PRIOR FILING DATE: 1999-01-25

Publication No. US20060177440A1

GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/11/328,483  
PRIOR FILING DATE: 2006-01-09  
PRIOR APPLICATION NUMBER: US/11/064,174  
PRIOR FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 167  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH34  
US-11-328-483-167

Query Match 86.4%; Score 472.5; DB 7; Length 108;  
Best Local Similarity 87.9%; Pred. No. 6,8e-37;  
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLMWYQKPGKAPKLLIYASNSLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITTCRASQISSTYLMWYQKPGKAPKLLIYASNSLQSGVPSRF 61  
QY 61 SGGSGTEFTLTISNQEPDPAASYCOOSYTT-LYTGSGTKLEIKR 106  
DB 62 SGGSGTEFTLTISNQEPDPAASYCOOSYTPPTTGGTKLEIKR 108

RESULT 10  
US-11-328-483-38  
Sequence 38, Application US/11328483  
Publication No. US20060177440A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/11/328,483  
PRIOR FILING DATE: 2006-01-09  
PRIOR APPLICATION NUMBER: US/11/064,174  
PRIOR FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I07  
US-11-328-483-38

Query Match 86.3%; Score 472; DB 7; Length 107;  
Best Local Similarity 86.8%; Pred. No. 7.5e-37;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLMWYQKPGKAPKLLIYASNSLQSGVPSRF 60

DB 2 ELTQSPSSLSASVGDVVTITTCRASQISSTYLMWYQKPGKAPKLLIYASNSLQSGVPSRF 61  
QY 61 SGGSGTEFTLTISNQEPDPAASYCOOSYTTLYTGSGTKLEIKR 106  
DB 62 SGGSGTEFTLTISNQEPDPAASYCOOSYTPPTTGGTKLEIKR 107

RESULT 11  
US-11-328-483-39  
Sequence 39, Application US/11328483  
Publication No. US20060177440A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/11/328,483  
PRIOR FILING DATE: 2006-01-09  
PRIOR APPLICATION NUMBER: US/11/064,174  
PRIOR FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 39  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain I08  
US-11-328-483-39

Query Match 86.3%; Score 472; DB 7; Length 107;  
Best Local Similarity 86.8%; Pred. No. 7.5e-37;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRASQISSTYLMWYQKPGKAPKLLIYASNSLQSGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITTCRASQISSTYLMWYQKPGKAPKLLIYASNSLQSGVPSRF 61  
QY 61 SGGSGTEFTLTISNQEPDPAASYCOOSYTTLYTGSGTKLEIKR 106  
DB 62 SGGSGTEFTLTISNQEPDPAASYCOOSYTPPTTGGTKLEIKR 107

RESULT 12  
US-11-328-483-162  
Sequence 162, Application US/11328483  
Publication No. US20060177440A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/11/328,483  
PRIOR FILING DATE: 2006-01-09  
PRIOR APPLICATION NUMBER: US/11/064,174  
PRIOR FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380  
PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 162  
LENGTH: 107  
TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) antibody clone SH24  
US-11-328-483-162

Query Match  
Best Local Similarity 86.3%; Score 472; DB 7; Length 107;  
Pred. No. 7.5e-37;  
Matches 90; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 61  
61 SSGSGTEFTLTISNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 62 TSSGSGTDFLTITISLQPEDFATYYCOQSYTTLTYFGSGTKLEIKR 107

## RESULT 13

US-11-337-300-41  
Sequence 41, Application US/11337300  
Publication No. US20060121580A1  
GENERAL INFORMATION:  
APPLICANT: Crucell Holland B.V.  
APPLICANT: ter Meulen, Jan H.  
APPLICANT: De Kruif, Cornelis A.  
APPLICANT: van den Brink, Edward N.  
APPLICANT: Goudemilc, Jaap  
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
FILE REFERENCE: 0091 WO 00 ORD  
CURRENT APPLICATION NUMBER: US/11/337,300  
CURRENT FILING DATE: 2006-01-20  
NUMBER OF SEQ ID NOS: 478  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 41  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Variable light chain of SC03-001, SC03-002, SC03-003, SC03-004, S  
OTHER INFORMATION: C03-005, SC03-007, SC03-008, SC03-009, SC03-010, SC03-013, SC03-0  
OTHER INFORMATION: 14, SC03-016 and SC03-018  
US-11-337-300-41

Query Match  
Best Local Similarity 86.1%; Score 471; DB 7; Length 106;  
Pred. No. 9.2e-37;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 60  
DB 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 60  
QY 61 SSGSGTEFTLTISNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 61 SSGSGTDFLTITISLQPEDFATYYCOQSYTTLTYFGSGTKLEIKR 106

## RESULT 14

US-11-328-483-158  
Sequence 158, Application US/11328483  
Publication No. US20060177440A1  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-42U2  
CURRENT APPLICATION NUMBER: US/11/328,483  
CURRENT FILING DATE: 2006-01-09  
PRIOR APPLICATION NUMBER: US/11/064,174  
PRIOR FILING DATE: 2005-02-22  
PRIOR APPLICATION NUMBER: US/09/240,274  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/081,380

PRIOR FILING DATE: 1998-04-10  
PRIOR APPLICATION NUMBER: 60/028,550  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 158  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
OTHER INFORMATION: anti-Rh(D) antibody clone SH16  
US-11-328-483-158

Query Match  
Best Local Similarity 86.1%; Score 471; DB 7; Length 107;  
Pred. No. 9.3e-37;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 60  
DB 2 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 61  
QY 61 SSGSGTEFTLTISNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 62 SSGSGTDFLTITISLQPEDFATYYCOQSYTTLTYFGSGTKLEIKR 107

## RESULT 15

US-11-337-300-47  
Sequence 47, Application US/11337300  
Publication No. US20060121580A1  
GENERAL INFORMATION:  
APPLICANT: Crucell Holland B.V.  
APPLICANT: ter Meulen, Jan H.  
APPLICANT: De Kruif, Cornelis A.  
APPLICANT: van den Brink, Edward N.  
APPLICANT: Goudemilc, Jaap  
TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof  
FILE REFERENCE: 0091 WO 00 ORD  
CURRENT APPLICATION NUMBER: US/11/337,300  
CURRENT FILING DATE: 2006-01-20  
NUMBER OF SEQ ID NOS: 478  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: SC03-001  
US-11-337-300-47

Query Match  
Best Local Similarity 86.1%; Score 471; DB 7; Length 243;  
Pred. No. 2.2e-36;  
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 60  
DB 135 ELTQSPSSLSASVGDVVTITCRAROSISTYLMWYQKPKAPKLLIWSASNLQGVPSRF 194  
QY 61 SSGSGTEFTLTISNLOFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106  
DB 195 SSGSGTDFLTITISLQPEDFATYYCOQSYTTLTYFGSGTKLEIKR 240

Search completed: August 30, 2006, 00:52:01  
Job time: 13.5273 secs

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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:02 ; Search time 95.2394 Seconds  
(without alignments)  
508,875 Million cell updates/sec

Title: US-10-027-725A-12

Sequence: 1 ELTQSPSSVSASVDRVTIT.....QQANSPPYTGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	96.0	106	5	ABG30450
2	518	94.4	233	7	ABB03713
3	518	94.4	233	7	ADB72874
4	499	90.9	107	10	AEF11002
5	499	90.9	129	10	AEF11041
6	498	90.7	115	10	AEF11041
7	493	89.8	107	9	ADY26765
8	493	89.8	115	10	AEF11041
9	491	89.4	107	8	ADP22406
10	491	89.4	129	9	ADZ57711
11	490	89.3	107	10	AEF11030
12	490	89.3	129	10	AEF11044
13	489	89.1	236	9	ADZ57703
14	488	88.9	108	9	AEA41079
15	487	88.7	107	8	ADP22216
16	486	88.5	108	9	AEA41087
17	486	88.5	115	10	AEF11031
18	485	88.3	107	5	ABB07237
19	485	88.3	107	9	AEA08942
20	485	88.3	249	10	AEF11041
21	485	88.3	249	10	AEF11041
22	484	88.2	223	6	ABJ36940
23	483	88.0	129	9	ADZ57710

24	482	87.8	155	10	AEF94857	AEF94857 Antibody
25	482	87.8	155	10	AEF94834	AEF94834 Antibody
26	482	87.8	234	7	ADM47073	ADM47073 Mouse ant
27	481	87.6	129	9	ADZ57708	ADZ57708 Germline
28	480	87.4	107	10	AEF73662	AEF73662 Human rab
29	480	87.4	249	10	AEF73761	AEF73761 Human ant
30	479	87.2	107	7	ADP03922	ADP03922 Murine-ex
31	479	87.2	107	7	ADP03994	ADP03994 Murine-ex
32	478	87.1	107	4	AA665571	AA665571 Antino aci
33	478	87.1	107	7	ADP03924	ADP03924 Murine-ex
34	478	87.1	107	7	ADP03989	ADP03989 Murine-ex
35	478	87.1	107	7	ADP03921	ADP03921 Murine-ex
36	478	87.1	244	5	ABP45870	ABP45870 Human Bly
37	478	87.1	244	9	ADG96697	ADG96697 Single ch
38	478	87.1	244	9	ADG96697	ADG96697 Single ch
39	477	86.9	107	9	ADX15508	ADX15508 Human ant
40	477	86.9	107	9	ADX88404	ADX88404 Human ant
41	477	86.9	129	9	ADX98252	ADX98252 Human ant
42	477	86.9	212	8	ADF76324	ADF76324 M16-L 1lg
43	475.5	86.6	116	10	AEF01345	AEF01345 Kallikrei
44	475	86.5	107	10	AEF73646	AEF73646 Human rab
45	475	86.5	236	5	AU74297	AU74297 Anti-Huma

## ALIGNMENTS

RESULT 1	ABG30450	standard; protein; 106 AA.
ID	ABG30450	
XX	ABG30450	
AC	ABG30450	
XX	21-OCT-2002	(first entry)
DT	21-OCT-2002	
XX	Human Igs Fab clone 100 light chain protein.	
XX	Human, fab; antiallergic; vaccine; grass pollen; phi p 2;	
KM	timothy grass pollen allergen; passive immunotherapy.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	Region	1..21
FT	Region	/note="FR1 region"
FT	Region	/note="FR1 region"
FT	Region	22..32 "CDR1 region"
FT	Region	/note="CDR1 region"
FT	Region	33..47
FT	Region	/note="FR2 region"
FT	Region	48..54
FT	Region	/note="CDR2 protein"
FT	Region	55..86 "FR3 region"
FT	Region	/note="FR3 region"
FT	Region	87..95
FT	Region	/note="CDR2 region"
FT	Region	96..104
FT	Region	/note="FR4 region"
PN	WO200253595-A1	
PD	11-JUL-2002	
XX	27-DEC-2001	2001WO-SE002908.
XX	27-DEC-2001	2000SE-00004892.
XX	29-DEC-2000	2000SE-00004892.
XX	(PHAA ) PHARMACIA DIAGNOSTICS AB.	
XX	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX	WPI; 2002-583604/62.	

DR N-PSDB; ABX89642.  
XX  
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising  
PT variable region of group 2 allergen-specific-human IgE Fabs, useful for  
PT diagnosing or passive immunotherapy of type I allergy, for environmental  
PT allergen detection.  
XX  
PS Disclosure; Page 41; 45pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of group 2  
CC allergen-specific human IgE Fabs and methods for their use. The proteins  
CC of the invention may have anti-allergic activities and may be used as a  
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE  
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group  
CC 2 allergen-specific Fabs of the invention may be useful for environmental  
CC allergen detection and for standardisation of allergen extracts. The Fabs  
CC - or a vaccine against a type I allergy is useful for passive  
CC immunotherapy of type I allergy, it is also useful for diagnosing a type  
CC I allergy. The allergen-specific Fabs of the invention are useful for  
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are  
CC also useful for identification of group 2 allergen-containing pollen and  
CC may be used for blocking the binding of grass pollen allergic patients  
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG  
CC Fab, clone 100 light chain protein of the invention  
XX  
SQ Sequence 106 AA;  
XX  
Query Match 96.0%; Score 527; DB 5; Length 106;  
Best Local Similarity 97.2%; Pred. No. 8.1e-30;  
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1 ELTQSPSSVSASVGDRTYITTCRASQGISWLAWYQHQPGRKPKLLIYSASSLSQGVPSRF 60  
Db 1 ELTQSPSSVSASVGDRTYITTCRASQGISWLAWYQHQPGRKPKLLIYSASSLSQGVPSRF 60  
XX  
QY 61 SSGSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGQTKVEIKR 106  
Db 61 SSGSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGQTKVEIKR 106  
XX  
RESULT 2  
AAB03713  
ID AAB03713 standard; protein; 233 AA.  
XX  
AC AAB03713;  
XX  
DT 04-OCT-2000 (first entry)  
XX  
DE Immunoglobulin kappa amino acid sequence fragment.  
XX  
KW Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;  
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;  
KW Immunoglobulin kappa; Igk.  
XX  
XX Unidentified.  
XX  
XX OS US6048704-A.  
XX  
XX PN US6048704-A.  
XX  
XX PD 11-APR-2000.  
XX  
XX PF 07-MAR-1997; 97US-00812586.  
XX  
XX PR 07-MAR-1996; 96US-0012976P.  
XX  
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX PI Tilson MD;  
XX  
XX DR WPI; 2000-316895/27.  
XX  
PT Isolated microfibrillar protein for alleviating abdominal aortic aneurysm  
PT disease is purified from human aortic tissue and binds immunoreactively  
PT with immunoglobulin.

XX  
PS Example 3; Col 29-31; 70pp; English.  
XX  
CC The present invention relates to an isolated microfibrillar protein of  
CC approximately 40kD. The protein is isolated from human aortic tissue and  
CC binds immunoreactively with immunoglobulin purified from human abdominal  
CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic  
CC aneurysm-associated antigenic protein (AAP). The protein is capable of  
CC forming a disulphide bonded dimer. The protein is immunoreactive with  
CC human kappa immunoglobulin. Also included in the invention are  
CC recombinantly produced human AAP proteins. AAP shows regions of homology  
CC with the bovine microfibril associated glycoprotein WFAP-4 and also with  
CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful  
CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the  
CC presence of AAA-associated immunoglobulin bound to the human aortic  
CC tissue. Antibodies directed against AAP can be used to detect AAA  
CC disease. The recombinant protein can be used to induce tolerance to  
CC antigenic AAP protein in the subject e.g. human. This sequence represents  
CC an immunoglobulin kappa amino acid sequence. The sequence shares homology  
CC with the AAP of the invention, it was used to identify and characterise  
CC AAP  
XX  
SQ Sequence 233 AA;  
XX  
Query Match 94.4%; Score 518; DB 3; Length 233;  
Best Local Similarity 96.2%; Pred. No. 6.9e-29;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 1 ELTQSPSSVSASVGDRTYITTCRASQGISWLAWYQHQPGRKPKLLIYSASSLSQGVPSRF 60  
Db 23 ELTQSPSSVSASVGDRTYITTCRASQGISWLAWYQHQPGRKPKLLIYSASSLSQGVPSRF 82  
XX  
QY 61 SSGSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGQTKVEIKR 106  
Db 83 SSGSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGGQTKVEIKR 128  
XX  
RESULT 3  
ADB72874  
ID ADB72874 standard; protein; 233 AA.  
XX  
AC ADB72874;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.  
XX  
KW Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;  
KW AAA-associated immunoglobulin 40kDa protein.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US6537769-B1.  
XX  
XX PD 25-MAR-2003.  
XX  
XX PF 28-MAR-2000; 2000US-00535832.  
XX  
XX PR 07-MAR-1996; 96US-0012976P.  
XX  
XX PR 07-MAR-1997; 97US-00812586.  
XX  
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX PI Tilson MD;  
XX  
XX DR WPI; 2003-687181/65.  
XX  
XX PT Purified protein useful in diagnosing abdominal aortic aneurysm disease  
XX in subject, e.g. human, contains specified amino acids.  
XX  
XX PS Disclosure; Col 73-74; 67pp; English.  
XX  
CC The present invention relates to the isolation of a protein approximately



CC 40kDa which is purified from human aortic tissue. The protein is  
 CC immunoreactive with abdominal aortic aneurysms (AAA)-associated  
 CC immunoglobulin. The protein is useful for diagnosing AAA disease in a  
 CC subject, e.g. human, by administering the protein or a composition  
 CC comprising the protein. The inventive protein is capable of forming a  
 CC disulphide-bonded dimer of 80 kDa. The present sequence of unknown  
 CC function is given in the Sequence Listing but is not mentioned elsewhere  
 CC in the specification.

XX Sequence 233 AA:

SO Query Match 94.4%; Score 518; DB 7; Length 233;  
 Best Local Similarity 96.2%; Pred. No. 6.9e-29;  
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMWYQHKGKAPKLLIYSSLSQGVPSRF 60  
 Db 23 ELTQSPSSVSASVGDRTVITTCRASQGISWLMWYQHKGKAPKLLIYSSLSQGVPSRF 82

Qy 61 SGSGYGTDFSLTISLQPEDSATYVCOQANSFPYTFGQGTKEIKR 106  
 Db 83 SGSGGTDFSLTISLQPEDSATYVCOQANSFPYTFGQGTKEIKR 128

RESULT 4  
 ID AEF11002 standard; protein; 107 AA.

XX AEF11002;  
 XX 09-MAR-2006 (first entry)

DE Human clone 3D8 antibody group I variable light chain region.

XX light chain variable region; monoclonal antibody therapy;  
 KW antibody identification; antitoxin; antibody; epitope mapping;  
 KM antiidiartheic; antibacterial; antiinflammatory; gastrointestinal disease;  
 KM clostridium difficile infection; pseudomembranous colitis; inflammation.

XX Homo sapiens.

OS Key Location/Qualifiers  
 FH Region 24..34  
 FT Region /label= CDR1  
 FT Region 50..56  
 FT Region /label= CDR2  
 FT Region 89..97  
 FT Region /label= CDR3

PN US2005287150-A1.

PD 29-DEC-2005.

PF 04-FEB-2005; 2005US-00051453.

PR 06-FEB-2004; 2004US-0542357P.

PR 28-SEP-2004; 2004US-0613854P.

PA (UYMA-) UNITV MASSACHUSETTS.

PA (MEDA-) MEDAREX INC.

PI Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HJ,

PI Lowy I, Mandell R, Molrine D, Thomas WD, Zhang H,

DR WPI; 2006-065655/07.

DR N-PSDB; AEF11033.

XX New human monoclonal antibody or its antigen binding portion that  
 PT specifically binds to an exotoxin of Clostridium difficile; useful in  
 PT preparing a composition for treating a Clostridium difficile-associated  
 PT disorder in a mammal.  
 XX Claim 20; SEQ ID NO 4; 98pp; English.

XX The present sequence of the variable light chain (Vkappa) region of a  
 CC novel isolated human monoclonal antibody produced by hybridoma clone 3D8  
 CC and encoded by the nucleic acid of SEQ ID NO. 35 AEF11033, specifically  
 CC binds to toxin A, an exotoxin of Clostridium difficile and is used in the  
 CC current invention in a method of treating C. difficile-associated disease  
 CC (CDAD) in a subject. The antibody or its antigen binding portion of the  
 CC invention inhibits CDAD in vivo. The antibody or its antigen binding  
 CC portion protects from or inhibits C. difficile-mediated colitis,  
 CC antibiotic-associated colitis, C. difficile-mediated pseudomembranous  
 CC colitis (PMC), C. difficile-mediated diarrhea in a subject and inhibits  
 CC relapse of C. difficile-mediated disease. The variable light chain region  
 CC of the antibody or its antigen-binding portion comprises three  
 CC complementarily determining regions (CDRs; SEQ ID Nos. 16-18). The  
 CC antibody or its antigen binding portion specifically binds to an epitope  
 CC consisting of the C-terminal half of toxin B and the toxin B receptor  
 CC domain, between amino acids 1777-2366 of the toxin B receptor domain. The  
 CC antibody or its antigen binding portion specifically binds to an epitope  
 CC within the C-terminal receptor binding domain of toxin A, between amino  
 CC acids 1853-2710 of toxin A. The antibody or its antigen binding portion  
 CC specifically binds to toxin A or B with a KD of less than 20 microm. The  
 CC antibody or its antigen binding portion comprises a heavy chain variable  
 CC region that is the product of or derived from a human VH 3-33 gene and  
 CC comprises a light chain variable region that is the product of or derived  
 CC from a human Vkappa gene consisting of VK L19, VK L6 or VK L15. The  
 CC antibody or its antigen binding portion comprises a heavy chain variable  
 CC region that is the product of or derived from a human VH 5-51 gene and  
 CC comprises a light chain variable region that is the product of or derived  
 CC from a human VK A27 gene. The antibody or its antigen-binding portion  
 CC comprises an effector or an Fc domain. The antibody or its antigen-  
 CC binding portion is a single-chain antibody or a Fab fragment. The  
 CC antibody or its antigen-binding portion is administered in combination  
 CC with a second agent. The second agent is a second human monoclonal  
 CC antibody or its antigen-binding portion, a C. difficile vaccine, and/or  
 CC an antibiotic such as vancomycin or metronidazole. The antibody or  
 CC antigen binding portion thereof specifically binds to C. difficile toxin  
 CC A and the second human monoclonal antibody or antigen binding portion  
 CC thereof specifically binds to Clostridium difficile toxin B.

SO Sequence 107 AA:

Query Match 90.9%; Score 499; DB 10; Length 107;  
 Best Local Similarity 91.4%; Pred. No. 7.5e-28;  
 Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMWYQHKGKAPKLLIYSSLSQGVPSRF 60  
 Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMWYQHKGKAPKLLIYSSLSQGVPSRF 62

Qy 61 SGSGYGTDFSLTISLQPEDSATYVCOQANSFPYTFGQGTKEIKR 105  
 Db 63 SGSGGTDFSLTISLQPEDSATYVCOQANSFPYTFGQGTKEIKR 107

RESULT 5

ID AEF11041 standard; protein; 129 AA.

XX AEF11041;

DT 09-MAR-2006 (first entry)

DE Human clone 3D8 antibody full length group I Vkappa region.

XX light chain variable region; monoclonal antibody therapy;  
 KW antibody identification; antitoxin; antibody; epitope mapping;  
 KM antiidiartheic; antibacterial; antiinflammatory; gastrointestinal disease;  
 KM clostridium difficile infection; pseudomembranous colitis; inflammation.

XX Homo sapiens.

OS Key Location/Qualifiers  
 FH Key 1..22  
 FT Peptide

FT /label= leader\_peptide  
 FT 23..129  
 FT /label= Mature anti-C. difficile toxin A antibody\_group\_1  
 FT /label= variable\_light\_chain\_region  
 FT 46..56  
 FT /label= CDR1  
 FT 72..78  
 FT /label= CDR2  
 FT 111..119  
 FT /label= CDR3  
 FT  
 FT US2005287150-A1.  
 FT  
 FT 29-DEC-2005.  
 FT  
 FT 04-FEB-2005; 2005US-00051453.  
 FT  
 FT 06-FEB-2004; 2004US-0542357P.  
 FT 28-SEP-2004; 2004US-0613854P.  
 FT  
 FT (UYMA-) UNIV MASSACHUSETTS.  
 FT (MEDA-) MEDAREX INC.  
 FT  
 FT Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HJ;  
 FT Lowy I, Mandell R, Molrine D, Thomas WD, Zhang H;  
 FT  
 FT WPI; 2006-065655/07.  
 FT  
 FT New human monoclonal antibody or its antigen binding portion that  
 FT specifically binds to an exotoxin of Clostridium difficile, useful in  
 FT preparing a composition for treating a Clostridium difficile-associated  
 FT disorder in a mammal.  
 FT  
 FT Disclosure; SEQ ID NO 43; 98bp; English.  
 FT  
 FT The present full length sequence is that of the variable light chain  
 FT (Vkappa) region of a novel isolated human monoclonal antibody produced by  
 FT hybridoma clone 3D8 (group I) which specifically binds to toxin A, an  
 FT exotoxin of Clostridium difficile, and is used in the current invention  
 FT in a method of treating C. difficile-associated disease (CDAD) in a  
 FT subject. The antibody or its antigen binding portion of the invention  
 FT inhibits CDAD in vivo. The antibody or its antigen binding portion  
 FT protects from or inhibits C. difficile-mediated colitis, antibiotic-  
 FT associated colitis, C. difficile-mediated pseudomembranous colitis (PMC),  
 FT C. difficile-mediated diarrhea in a subject and inhibits release of C.  
 FT difficile-mediated disease. The variable light chain region of the  
 FT antibody or its antigen-binding portion comprises three complementarity  
 FT determining regions (CDRs; SEQ ID NOs. 16-18). The antibody or its  
 FT antigen binding portion specifically binds to an epitope consisting of  
 FT the C-terminal half of toxin B and the toxin B receptor domain, between  
 FT amino acids 1777-2366 of the toxin B receptor domain. The antibody or its  
 FT antigen binding portion specifically binds to an epitope within the C-  
 FT terminal receptor binding domain of toxin A, between amino acids 1853-  
 FT 2710 of toxin A. The antibody or its antigen binding portion specifically  
 FT binds to toxin A or B with a KD of less than 20 microm. The antibody or  
 FT its antigen binding portion comprises a heavy chain variable region that  
 FT is the product of or derived from a human VH 3-33 gene and comprises a  
 FT light chain variable region that is the product of or derived from a  
 FT human Vkappa gene consisting of VK L19, VK L6 or VK L15. The antibody or  
 FT its antigen binding portion comprises a heavy chain variable region that  
 FT is the product of or derived from a human VH 5-51 gene and comprises a  
 FT light chain variable region that is the product of or derived from a  
 FT human VK A27 gene. The antibody or its antigen-binding portion comprises  
 FT an effector or an Fc domain. The antibody or its antigen-binding portion  
 FT is a single-chain antibody or a Fab fragment. The antibody or its antigen  
 FT -binding portion is administered in combination with a second agent. The  
 FT second agent is a second human monoclonal antibody or its antigen-binding  
 FT portion, a C. difficile vaccine, and/or an antibiotic such as vancomycin  
 FT or metronidazole. The antibody or antigen binding portion thereof  
 FT specifically binds to C. difficile toxin A and the second human  
 FT monoclonal antibody or antigen binding portion thereof specifically binds  
 FT to Clostridium difficile toxin B.

SO Sequence 129 AA;  
 Query Match 90.9%; Score 499; DB 10; Length 129;  
 Best Local Similarity 91.4%; Pred. No. 8.9e-28;  
 Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ELTQSPSSVSASVGDVRVITTCRASQGISISWLMAYOHQPKAKLLIYASNSIQSGVPSRF 60  
 DB 25 QMTQSPSSVSASVGDVRVITTCRASQGISISWLMAYOHQPKAKRLIYAASISQSGVPSRF 84  
 QY 61 SGSGYGTDFSLTITSSIQFEDSATIYCOQANSFPYFGQTKYKIK 105  
 DB 85 SGSGSGTDFSLTITSSIQFEDFATYCOQANSFPWTFGQTKYKIK 129  
 RESULT 6  
 AEG01253  
 ID AEG01253 standard; protein, 115 AA.  
 XX  
 AC AEG01253;  
 XX  
 DT 20-APR-2006 (first entry)  
 XX  
 XX Kalikrein 1 antibody light chain variable region SEQ ID NO:1080.  
 XX  
 XX Antibody; light chain variable region; kalikrein 1; therapeutic;  
 KW Antithrombotic; Respiratory-Gen.; Neuroprotective; Antipsoriatic;  
 KW Antithrombotic; Antiarthritic; Osteopathic; Antiallergic;  
 KW Antinflammatory; Gastrointestinal-Gen.; Antidiabetic; Cytostatic;  
 KW Cardiovascular-Gen.; Urologic; Angiogenesis Inhibitor; Asthma;  
 KW Chronic obstructive pulmonary disease; Multiple sclerosis; Psoriasis;  
 KW Rheumatoid arthritis; Osteoarthritis; Allergic rhinitis; Sinusitis;  
 KW Inflammatory bowel disease; Diabetes; Pancreatitis;  
 KW Interstitial cystitis; Neoplasm; Pancreatic ductal adenocarcinoma; Tumor;  
 KW Angiogenesis; Cardiovascular disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WC02006017538-A2.  
 XX  
 PD 16-FEB-2006.  
 XX  
 PF 03-AUG-2005; 2005WO-US027493.  
 XX  
 PR 03-AUG-2004; 2004US-0598506P.  
 PR 04-OCT-2004; 2004US-0615721P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 PA  
 PI Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q;  
 XX  
 XX WPI; 2006-184027/19.  
 DR  
 XX Novel protein comprising immunoglobulin heavy and light chain variable  
 FT domain sequences, capable of inhibiting human tissue kallikrein-1  
 FT enzymatic activity, useful for treating human tissue kallikrein-1  
 FT associated disorder, e.g. asthma.  
 FT  
 FT Example; SEQ ID NO 1080; 178bp; English.  
 PS  
 XX The invention relates to a protein (I) comprising an immunoglobulin heavy  
 CC chain (HC) variable domain sequence and an immunoglobulin light chain  
 CC (LC) variable domain sequence, where the HC variable domain sequence and  
 CC the LC variable domain sequence form an antigen binding site binding to  
 CC human tissue kallikrein-1 (hK1) and inhibiting enzymatic activity of hK1.  
 CC Also included is a pharmaceutical composition (II) comprising the protein  
 CC and carrier. The protein is useful for treating or preventing an hK1  
 CC associated disorder, which involves administering (I) to a subject to  
 CC treat or prevent the hK1 associated disorder. The disorder is chosen from  
 CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,  
 CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,  
 CC inflammatory bowel diseases, immune mediated diabetes, acute pancreatitis,  
 CC interstitial cystitis or neoplastic disorder. The disorder

is asthma and the asthma is allergic or non-allergic asthma. The disorder is a neoplastic disorder, which is metastatic pancreatic adenocarcinoma or tumor angiogenesis. The method further involves administering a second agent that modulates angiogenesis. The second agent is an anti-vascular endothelial growth factor (VEGF) antibody or its antigen binding CC fragment. The protein is useful for modulating an hK1 activity, for CC detecting the presence of an hK1 protein in vitro, for detecting the CC presence of an hK1 in vivo in a human subject, and for reducing CC angiogenesis associated with cardiovascular disorders. The present CC sequence is the light chain variable region of an anti-kallikrein 1 CC antibody of the invention.

Query Match	90.7%	Score 498	DB 10	Length 115
Best Local Similarity	90.6%	Pred. No. 9.4e-28		
Matches 96	Conservative	6	Mismatches 4	Indels 0
				Gaps 0

QY 1 ELTQSPSSVASVGDRTYITICRASQGISWILAWYQHCPGAPLTLIYASLSLOSQVPSRF 60  
:::|||||  
Db 5 QMTQSPSSVASVGDRTYITICRASQGISWILAWYQKPKRAPLTLIYASLSLOSQVPSRF 64  
  
QY 61 SSGSGYCTMDESLTSSLPEDSATYYCOQANSFYTTGGCGTKVIR 106  
:::|||||  
Db 65 SSGSGSGTDFLTLLTSSLPEDFATYYCOQANSFYTTGGCGTKVIR 110

RESULT 7	
ADY26765	
ID	ADY26765 standard; protein; 107 AA.

DT 19-MAY-2005 (first entry)

DE	Anti-NGF-antibody light chain variable region	SEQ ID NO 80.	-
XX			
KM	analgesic; gene therapy; antibody engineering; pharmaceutical; pain		
KW	neurological disease; NGF; nerve growth factor;		
KW	light chain variable region.		

OS	Homo sapiens.
XX	
PN	W02005019266-A2.

PD	03-MAR-2005.
XX	
PF	15-JUL-2004; 2004WO-US022876.

PR 15-JUL-2003; 2003US-0487431P.

PA (AMGE-) AMGEN INC.

PI Wild KD, Treanor JS, Huang H, Inoue H, Zhang TJ, Martin F;

DR WPI: 2005-202606/21.

PT New human anti-nerve growth factor (NGF) neutralizing antibodies useful  
PT for manufacturing a medicament for treating painful disorders (e.g. acute  
PT pain) or conditions associated with increased expression or sensitivity  
PT to NGF.

PS Claim 33; SEQ ID NO 80; 190pp; English.

CC The invention describes an isolated human antibody that interacts with o  
CC binds specifically to human nerve growth factor (NGF) and neutralize the  
CC function of NGF. Also described are: methods of treating a condition  
CC caused by increased expression of NGF or increased sensitivity to NGF in  
CC a patient; methods for detecting NGF in a biological sample; an NGF  
CC specific binding agent comprising any of the 55 amino acid sequences  
CC comprising, for e.g., 123, 107 or 14 amino acids, as mentioned in the  
CC specification, and where the binding agent can bind to NGF; a  
CC pharmaceutical composition comprising a pharmaceutical carrier and a

CC therapeutic amount of the antibody or binding agent cited above; or a  
CC medicament for treating a painful disorder or condition associated with  
CC increased expression of NGF or increased sensitivity to NGF, the  
CC medicament comprising a pharmaceutical amount of a monoclonal antibody or  
CC its immunologically functional immunoglobulin fragment, or pharmaceutical  
CC salts of the monoclonal antibody or the fragment, where the monoclonal  
CC antibody is at least one of the monoclonal antibody cited above, and a  
CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or  
CC polynucleotide that encodes the above antibody or binding agent; an  
CC isolated cell line that produces the above antibody or binding agent; an  
CC expression vector comprising the above polynucleotide; and a host cell  
CC comprising the nucleic acid or expression vector. The composition  
CC (including the antibody) and methods are useful for manufacturing a  
CC medicament for treating a painful disorder (e.g., acute pain, dental pain,  
CC or pain from trauma or cancer), or a condition associated with increased  
CC expression of NGF or increased sensitivity to NGF. This is the amino acid  
CC sequence of a human NGF antibody light chain variable region.

**SQ** Sequence 107 AA;

Query Match	89.8%	Score 493	DB 9	length 107
Best Local Similarity	90.5%	Pred. No.2e-27		
Matches 95; Conservative	6	Mismatches	4	Indels 0
				Gaps 0

```
QY      1 ELTSPSSVSASVGDRTITCRASGGISSWLAWQHOGCKAPKLLIYSASSLSQGVPSTRF    600
        ::|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       3 QMTSPSSVSASVGDRTITCRASGGISWLAWQHKGCKAPKLLIYAASSLSQGVPSTRF    622
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QY      61 SSGSGYGDPSLTITISSLQPEDSATYCCQANSFPYTFGGGTKEIK 105
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SSGSGGTDFTLTITISSLQPEDFATYCCQANSFPWTFGGGTKEIK 107
```

RESULT 8  
AEG01358  
ID AEG01358 standard; protein; 115 AA

AC AEG01358;

DT 20-APR-2006 (first entry)

DE Kallikrein 1 antibody light chain variable region SEQ ID NO:1185.

KW Antibody; light chain variable region; kallikrein 1; therapeutic;

KW Antirheumatic; Antiarthritic; Osteopathic; Antiallergic;

KW Cardiovascular-Gen.; uropathic; Angiogenesis Inhibitor; asthma;

KW rheumatoid arthritis; osteoarthritis; allergic rhinitis; sinusitis;

KW interstitial cystitis; neoplasm; pancreatic ductal adenocarcinoma; tumor;

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[illegible]

**XX**

PR . 04-OCT-2004; 2004US-0615721P.

PA (DYAX-) DYAX CORP.

PI Sexton DJ, Nixon A, Williams A, Ladner RC, Wu Q, et al.

DR WPI; 2006-184027/19.  
yy

PT Novel protein comprising immunoglobulin heavy and light chain variable domain sequences capable of inhibiting human tissue kallikrein-1

PT enzymatic activity, useful for treating human tissue kallikrein-1  
 associated disorder, e.g. asthma.  
 XX  
 XX Example; SEQ ID NO 1185; 178pp; English.  
 XX  
 CC The invention relates to a protein (I) comprising an immunoglobulin heavy  
 CC chain (HC) variable domain sequence and an immunoglobulin light chain  
 CC (LC) variable domain sequence, where the HC variable domain sequence and  
 CC the LC variable domain sequence form an antigen binding site binding to  
 CC human tissue kallikrein-1 (hKL) and inhibit enzymatic activity of hKL.  
 CC Also included is a pharmaceutical composition (II) comprising the protein  
 CC and carrier. The protein is useful for treating or preventing an hKL  
 CC associated disorder, which involves administering (i) to a subject to  
 CC treat or prevent the hKL associated disorder. The disorder is chosen from  
 CC asthma, chronic obstructive pulmonary disease (COPD), multiple sclerosis,  
 CC psoriasis, rheumatoid arthritis, osteoarthritis, rhinitis, sinusitis,  
 CC inflammatory bowel diseases, immune mediated diabetes, acute  
 CC pancreatitis, interstitial cystitis or neoplastic disorder. The disorder  
 CC is asthma and the asthma is allergic or non-allergic asthma. The disorder  
 CC is a neoplastic disorder, which is metastatic pancreatic adenocarcinoma  
 CC or tumor angiogenesis. The method further involves administering a second  
 CC agent that modulates angiogenesis. The second agent is an anti-vascular  
 CC endothelial growth factor (VEGF) antibody or its antigen binding  
 CC fragment. The protein is useful for modulating an hKL activity, for  
 CC detecting the presence of an hKL protein in vitro, for detecting the  
 CC presence of an hKL in vivo in a human subject, and for reducing the  
 CC angiogenesis associated with cardiovascular disorders. The present  
 CC sequence is the light chain variable region of an anti-kallikrein 1  
 CC antibody of the invention.  
 CC  
 XX Sequence 115 AA;  
 SQ  
 Query Match 89.8%; Score 493; DB 10; Length 115;  
 Best Local Similarity 89.6%; Pred. No. 2.1e-27;  
 Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTOSPSVASVDRVTITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 5 QMTOSPSVASVDRVTITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 64  
 QY 61 SSGSGYTDFTLITSLQFEDSATYTCQOANSFYTFGGGTVEIKR 106  
 Db 65 SSGSGYTDFTLITSLQFEDSATYTCQOANSFYTFGGGTVEIKR 110  
 RESULT 9  
 ID ADP22406 standard; protein; 107 AA.  
 XX  
 AC ADP22406;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 XX Human anti-TNFA antibody light chain variable region SEQ ID NO:312.  
 XX  
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KW antibacterial; antiinflammatory; antiprosclerotic; antineumatic;  
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;  
 KW neuroprotective; vasotrophic; antiapoptotic; TNFA antagonist;  
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KW prostate cancer; immuno-mediated inflammatory disease;  
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KW reestenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KW septic shock; cachexia; anorexia; multiple sclerosis.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2004050683-A2.  
 XX  
 XX 17-JUN-2004.

XX  
 PF 02-DEC-2003; 2003WO-US038281.  
 XX  
 XX 02-DEC-2002; 2002US-0430729P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 XX  
 PA Babcock JS, Kang JS, Poord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenchu K, Fagioni R, Senaldi G, Qiaojuan JS;  
 XX WPI, 2004-480601/45.  
 DR  
 XX  
 XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 XX Example 10; SEQ ID NO 312; 213pp; English.  
 XX  
 XX The present invention describes a human monoclonal antibody (I) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
 CC antibacterial, antiinflammatory, antiprosclerotic, antineumatic, eating-  
 CC disorder, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotrophic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of as  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, reestenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody light chain variable region, which is used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 107 AA;  
 SQ  
 Query Match 89.4%; Score 491; DB 8; Length 107;  
 Best Local Similarity 90.5%; Pred. No. 2.8e-27;  
 Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ELTOSPSVASVDRVTITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 60  
 Db 3 QMTOSPSVASVDRVTITCRASQGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRF 62  
 QY 61 SSGSGYTDFTLITSLQFEDSATYTCQOANSFYTFGGGTVEIKR 105  
 Db 63 SSGSGYTDFTLITSLQFEDSATYTCQOANSFYTFGGGTVEIKR 107  
 RESULT 10  
 ID AD257711 standard; protein; 129 AA.  
 XX  
 AC AD257711;  
 XX  
 DT 30-JUN-2005 (first entry)

```

DE  Gemline antibody L5WkL Jk1 light chain protein.
XX
XX  antibody engineering; cytostatic; vulnery; vasotropic; cardiant;
KW  monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;
KW  gastrointestinal ulcer; ischemia; transplant rejection;
KW  myocardial infarction; reperfusion injury; resenosis; angioplasty;
KW  vascular disease; cancer; retinopathy; endometriosis; arthritis;
KW  Alzheimer disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;
KW  antibody.
XX
XX  Homo sapiens.
XX
XX  GB2404660-A.
XX
XX  09-FEB-2005.
XX
XX  04-AUG-2004; 2004GB-00017384.
XX
XX  04-AUG-2003; 2003US-0492432P.
XX
XX  (PEIZ ) PEIZER PROD INC.
XX  (ABGE-) ABGENIX INC.
XX
XX  Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL;
XX  Jia X;
XX
XX  WPI; 2005-145169/16.
XX
XX  Human monoclonal antibody or antigen-binding portion that specifically
XX  binds to c-Met, useful for treating cancer by inhibiting c-Met or for
XX  promoting tissue regeneration and wound healing by activating c-Met.
XX
XX  Example 2; SEQ ID NO 20; 128pp; English.
XX
XX  The invention relates to a human monoclonal antibody (I) or its antigen-
XX  binding portion that specifically binds to c-Met, comprises a heavy chain
XX  having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is
XX  lysine and X4 is threonine, and a light chain having a fully defined
XX  sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both
XX  chains are without a signal sequence. All the sequences are fully defined
XX  in the specification. (I) is useful for the manufacture of a medicament
XX  for treating a hyperproliferative disorder in a subject, where the
XX  antibody or its portion is a c-Met antagonist. (I) is useful for
XX  manufacture of a medicament for promoting wound healing or tissue
XX  regeneration in a subject, where the antibody, antigen-binding portion or
XX  the composition activates c-Met. (I) which has a c-Met agonist activity
XX  is useful in tissue regeneration or wound healing (skin ulcers or gastric
XX  ulcers), or treating ischemia associated with kidney transplant
XX  rejection, for attenuating toxicity associated with cyclosporin treatment
XX  after transplant surgery, for treating myocardial infarction, cardiac
XX  ischemia due to reperfusion injury, restenosis after angioplasty or
XX  vascular disease. (I) which has a c-Met antagonist activity is useful
XX  for treating cancers of brain, lung, squamous cell, bladder, neck, liver,
XX  prostate, etc., proliferative vitreoretinopathy, proliferative diabetic
XX  retinopathy, endometriosis, and atherosclerosis, for inhibiting plaque
XX  formation in Alzheimer's disease, inhibiting cellular mitogenic
XX  responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas.
XX  (I) is useful for detecting c-Met in a biological sample in vitro or in
XX  vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has
XX  selectivity for c-Met that is at least 100 times greater than their
XX  selectivity for insulin like growth factor I receptor. This sequence
XX  corresponds to the amino acid sequence for a gemline antibody light
XX  chain used in the invention.
XX
XX  Sequence 129 AA;
XX
XX  Query Match      89.4%; Score 491; DB 9; Length 129;
XX  Best Local Similarity 90.5%; Pred. NO. 3.2e-27;
XX  Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0.

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Db	25	OMTQSPSSVASVSGDVRITTCRASQGISLWLMAYQOKGKAPKLIIYVASSLQSGVPSRF	84
Qy	61	SGSGYGTDPSELTISSIQFEEDSATYTCQOANSFPYFGGTVEIK	105
Db	85	SGSGSGTDFLTITISLQPEDFATYTCQOANSFPMTFGGTVEIK	129

RESULT 11

AFI1030	ID	AFI1030 standard; protein; 107 AA.
XX	AC	AFI1030;
XX	XX	09-MAR-2006 (first entry)
XX	DE	Human clone 3D8 antibody group IV variable light chain region.
KW	KW	light chain variable region; monoclonal antibody therapy;
KW	KW	antibody identification; antitoxic; antibiotic; epitope mapping;
KW	KW	antidiarrhetic; antibacterial; antiinflammatory; gastrointestinal disease
KW	KW	Clostridium difficile infection; pseudomembranous colitis; inflammation.
XX	OS	Homo sapiens.
XX	Key	Location/Qualifiers
FT	Region	24..34
FT	Region	/label= CDR1
FT	Region	50..56
FT	Region	/label= CDR2
FT	Region	89..97
FT	Region	/label= CDR3
XX	PN	US2005287150-A1.
XX	PD	29-DEC-2005.
XX	XX	04-FEB-2005; 2005US-00051453.
PF	PR	06-FEB-2004; 2004US-054237P.
PR	PR	28-SEP-2004; 2004US-0613854P.
XX	PA	(UYMA-) UNIV MASSACHUSETTS.
PA	PA	(MEDA-) MEDAREX INC.
XX	PI	Ambrosino D, Babcock GJ, Broering T, Graziano R, Hernandez HJ;
PI	PI	Lowy I, Mandell R, Molrine D, Thomas WD, Zhang H;
XX	DR	WPI; 2006-065655/07.
XX	XX	New human monoclonal antibody or its antigen binding portion that
PT	PT	specifically binds to an exotoxin of Clostridium difficile, useful in
PT	PT	preparing a composition for treating a Clostridium difficile-associated
PT	PT	disorder in a mammal.
XX	BS	Disclosure; SEQ ID NO 32; 98pp; English.
XX	XX	The present sequence of the variable light chain (V <sub>κ</sub> appa) region of a
CC	CC	novel isolated human monoclonal antibody produced by hybridoma clone 3D8
CC	CC	specifically binds to toxin A, an exotoxin of Clostridium difficile and
CC	CC	is used in the current invention in a method of treating C. difficile-
CC	CC	associated disease (CDAD) in a subject. The antibody or its antigen
CC	CC	binding portion of the invention inhibits CPAD in vivo. The antibody or
CC	CC	its antigen binding portion protects from or inhibits C. difficile-
CC	CC	mediated colitis, antibiotic-associated colitis, C. difficile-mediated
CC	CC	pseudomembranous colitis (PMC), C. difficile-mediated diarrhea in a
CC	CC	subject and inhibits relapse of C. difficile-mediated disease. The
CC	CC	variable light chain region of the antibody or its antigen-binding
CC	CC	portion comprises three complementarily determining regions (CDRs). The
CC	CC	antibody or its antigen binding portion specifically binds to an epitope
CC	CC	consisting of the C-terminal half of toxin B and the toxin B receptor
CC	CC	domain, between amino acids 1777-2366 of the toxin B receptor domain. The
CC	CC	antibody or its antigen binding portion specifically binds to an epitope
CC	CC	within the C-terminal receptor binding domain of toxin A. Between amino

CC acide 1853-2710 of toxin A. The antibody or its antigen binding portion  
 CC specifically binds to toxin A or B with a KD of less than 20 microm. The  
 CC antibody or its antigen binding portion comprises a heavy chain variable  
 CC region that is the product of or derived from a human VH 3-33 gene and  
 CC comprises a light chain variable region that is the product of or derived  
 CC from a human V kappa gene consisting of VK L19, VK L6 or VK L15. The  
 CC antibody or its antigen binding portion comprises a heavy chain variable  
 CC region that is the product of or derived from a human VH 5-51 gene and  
 CC comprises a light chain variable region that is the product of or derived  
 CC from a human VK A27 gene. The antibody or its antigen-binding portion  
 CC comprises an effector or an Fc domain. The antibody or its antigen-  
 CC binding portion is a single-chain antibody or a Fab fragment. The  
 CC antibody or its antigen-binding portion is administered in combination  
 CC with a second agent. The second agent is a second human monoclonal  
 CC antibody or its antigen-binding portion, a C. difficile vaccine, and/or  
 CC an antibiotic such as vancomycin or metronidazole. The antibody or  
 CC antigen binding portion thereof specifically binds to C. difficile toxin  
 CC A and the second human monoclonal antibody or antigen binding portion  
 CC thereof specifically binds to Clostridium difficile toxin B.

SO Sequence 107 AA;

Query Match 89.3%; Score 490; DB 10; Length 107;  
 Best Local Similarity 89.5%; Pred. No. 3.2e-27;  
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYOHQPGKAPKLLIYASASSLOGVPSRF 60  
 Db 3 QMTQSPSSVASVGDRTVITCRASQGISWLAHYOHQPGKAPKLLIYASASSLOGVPSRF 62  
 Qy 61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFYTFGQGTKEIK 105  
 Db 63 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFYTFGQGTKEIK 107

RESULT 12  
 AEF11044  
 ID AEF11044 standard; protein; 129 AA.

AC AEF11044;  
 XX  
 DT 09-MAR-2006 (first entry)  
 XX  
 XX Human clone 3D8 antibody full length group IV V kappa region.  
 XX  
 XX light chain variable region; monoclonal antibody therapy;  
 KW antibody identification; antitoxin; antibiotic; epitope mapping;  
 KW antidiarrheic; antibacterial; antiinflammatory; gastrointestinal disease;  
 KW Clostridium difficile infection; pseudomembranous colitis; inflammation.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= leader\_peptide  
 FT Protein 23..129  
 FT /label= Mature anti-C. difficile\_toxin\_A\_antibody\_group\_I  
 FT V variable\_light\_chain\_region  
 FT Region 46..56  
 FT /label= CDR1  
 FT Region 72..78  
 FT /label= CDR2  
 FT Region 111..119  
 FT /label= CDR3

US2005287150-A1.

29-DEC-2005.

04-FEB-2005; 2005US-00051453.

06-FEB-2004; 2004US-0542357P.  
 PR 28-SEP-2004; 2004US-0613854P.

XX (UYMA-) UNIV MASSACHUSETTS.  
 PA (MEDA-) MEDAREX INC.

PI Ambrosio D, Babcock GJ, Broering T, Graziano R, Hernandez HU;  
 PI Lowy I, Mandell R, Moline D, Thomas WD, Zhang H;  
 DR WPI; 2006-065655/07.

XX New human monoclonal antibody or its antigen binding portion that  
 PT specifically binds to an exotoxin of Clostridium difficile, useful in  
 PT preparing a composition for treating a Clostridium difficile-associated  
 PT disorder in a mammal.

PS Disclosure; SEQ ID NO 46; 98pp; English.

XX The present full length sequence is that of the variable light chain  
 CC (V kappa) region of a novel isolated human monoclonal antibody produced by  
 CC hybridoma clone 308 (group IV) which specifically binds to toxin A, an  
 CC exotoxin of Clostridium difficile, and is used in the current invention  
 CC in a method of treating C. difficile-associated disease (CDAD) in a  
 CC subject. The antibody or its antigen binding portion of the invention  
 CC inhibits CDAD in vivo. The antibody or its antigen binding portion  
 CC protects from or inhibits C. difficile-mediated pseudomembranous colitis (PMC),  
 CC associated colitis, C. difficile-mediated pseudomembranous colitis (PMC),  
 CC C. difficile-mediated diarrhea in a subject and inhibits relapse of C.  
 CC C. difficile-mediated disease. The variable light chain region of the  
 CC antibody or its antigen-binding portion comprises three complementarity  
 CC determining regions (CDRs). The antibody or its antigen binding portion  
 CC specifically binds to an epitope consisting of the C-terminal half of  
 CC toxin B and the toxin B receptor domain, between amino acids 1777-2266 of  
 CC the toxin B receptor domain. The antibody or its antigen binding portion  
 CC specifically binds to an epitope within the C-terminal receptor binding  
 CC domain of toxin A, between amino acids 1853-2710 of toxin A. The antibody  
 CC or its antigen binding portion specifically binds to toxin A or B with a  
 CC KD of less than 20 microm. The antibody or its antigen binding portion  
 CC comprises a heavy chain variable region that is the product of or derived  
 CC from a human VH 3-33 gene and comprises a light chain variable region  
 CC that is the product of or derived from a human V kappa gene consisting of  
 CC VK L19, VK L6 or VK L15. The antibody or its antigen binding portion  
 CC comprises a heavy chain variable region that is the product of or derived  
 CC from a human VH 5-51 gene and comprises a light chain variable region  
 CC that is the product of or derived from a human VK A27 gene. The antibody  
 CC or its antigen-binding portion comprises an effector or an Fc domain. The  
 CC antibody or its antigen-binding portion is a single-chain antibody or a  
 CC Fab fragment. The antibody or its antigen-binding portion is administered  
 CC in combination with a second agent. The second agent is a second human  
 CC monoclonal antibody or its antigen-binding portion, a C. difficile  
 CC vaccine, and/or an antibiotic such as vancomycin or metronidazole. The  
 CC antibody or antigen binding portion thereof specifically binds to C.  
 CC C. difficile toxin A and the second human monoclonal antibody or antigen  
 CC binding portion thereof specifically binds to Clostridium difficile toxin  
 CC B.

XX Sequence 129 AA;

SO Query Match 89.3%; Score 490; DB 10; Length 129;  
 Best Local Similarity 89.5%; Pred. No. 3.8e-27;  
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYOHQPGKAPKLLIYASASSLOGVPSRF 60  
 Db 25 QMTQSPSSVASVGDRTVITCRASQGISWLAHYOHQPGKAPKLLIYASASSLOGVPSRF 84  
 Qy 61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFYTFGQGTKEIK 105  
 Db 85 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFYTFGQGTKEIK 129

RESULT 13  
 AD257703  
 ID AD257703 standard; protein; 236 AA.



	CC	responsee, or for treating tumor, glioblastoma, sarcoma, or carcinomas.
	CC	(1) is useful for detecting c-Met in a biological sample in vitro or in
	CC	vivo, thus useful for diagnosing c-Met-expressing tumor. (1) has
	CC	selectivity for c-Met that is at least 100 times greater than c-Met
	CC	selectively for insulin like growth factor I receptor. This sequence
	CC	corresponds to the antibody 8.70.2 light chain used in the invention.
	XX	
SO	Sequence 236 AA;	
Query Match	89.1%; Score 489; DB 9; Length 236;	
Best Local Similarity	89.6%; Pred. No. 7.6e-27;	
Matches 95; Conservative	5; Mismatches 6; Indels 0; Gaps 0;	
DQ	1 ELTOSPESSASVAGDRTYITTCRASQGIGSSMLAWYOHOGKAPKLIIYSASSLSGSPERF 60 :::	
DB	25 QMTDSPESSASVAGDRTYITTCRASQGIGSSMLAWYOHOGKAPKLIIYSASSLSGSPERF 84 	
DQ	61 SGSGCYGFDFSLTITSLSLOPEDSATRYCCOANSFPYTFGGTGKVEIKR 106 	
DB	85 SGSGSGGTDFLTITISLQSEDPATRYCCQANSPFTTFPGTVEIKR 130 	
RESULT 14		
AEAA41079	ID AEAA41079 standard; protein; 108 AA.	
AC	AEAA41079;	
XX		
DT	28-JUL-2005 (first entry)	
XX		
DE	Germine V kappa L5, J kappa 3 amino acid sequence SEQ ID NO:109.	
XX		
KM	monoclonal antibody; macrophage colony stimulating factor inhibition;	
XX	light chain.	
OS	Unidentified.	
XX		
PN	GB2405873-A.	
XX		
PD	16-MAR-2005.	
PF	09-SEP-2004; 2004GB-00020044.	
PR	10-SEP-2003; 2003US-0502163P.	
XX		
PA	(WARIN ) WARNER LAMBERT CO LLC.	
PA	(ABGE-) ABGENIX INC.	
PI	Bedian V, Devalaraja MN, Low JE, Mobley JL, Kellermann S;	
PI	Foltz I, Haak-Frendescho M;	
XX		
DR	WPI; 2005-216576/23.	
PT	Novel humanized, chimeric or human monoclonal antibody e.g. 9.14.41 or	
PT	8.10.3F antibody that binds to and inhibits human macrophage colony	
PT	stimulating factor, useful for producing medicament for treating	
PT	rheumatoid arthritis.	
PS	Disclosure; SEQ ID NO 109; 155pp; English.	
XX		
CC	The invention relates to a humanized, chimeric or human monoclonal	
CC	antibody (I) or its antigen-binding portion that binds specifically to	
CC	and inhibits human macrophage colony stimulating factor (M-CSF). Also	
CC	described: (1) a polypeptide chosen from AEA41017, AEA41019, AEA41021,	
CC	AEA41023, AEA41025, AEA41027, AEA41028, AEA41029, AEA41030, AEA41031,	
CC	AEA41033, AEA41035, AEA41037, AEA41039, AEA41041, AEA41043, AEA41045,	
CC	AEA41047, AEA41049, AEA41051, AEA41053, AEA41054, AEA41055, AEA41056,	
CC	AEA41057, AEA41058, AEA41059, AEA41060, AEA41061, AEA41062, AEA41063,	
CC	AEA41064, AEA41065, AEA41066, AEA41067 and AEA41068, without a signal	
CC	sequence; (2) a composition (II) comprising (1) and a carrier; (3) an	
CC	isolated cell line (III) for producing (I) or its antigen-binding portion	
CC	or heavy or light chain of (I) or antigen-binding portions; and (4)	
CC	producing (I). (I) is useful for producing a medicament for treating a	

CC condition chosen from arthritis, psoriatic arthritis, rheumatoid  
 CC arthritis, gout, traumatic arthritis, rubella arthritis and acute  
 CC synovitis and other arthritic conditions, sepsis, septic shock, endotoxic  
 CC shock, gram negative sepsis, toxic shock syndrome, Alzheimer's disease,  
 CC stroke, neurociruma, asthma, adult respiratory distress syndrome,  
 CC cerebral malaria, tumor, and chronic pulmonary inflammatory disease,  
 CC preferably rheumatoid arthritis. The present sequence represents the  
 CC germline V kappa L5, J kappa 3 amino acid sequence, which is given in the  
 CC exemplification of the present invention.

XX Sequence 108 AA;  
 SQ

Query Match 88.7%; Score 487; DB 9; Length 107;  
 Best Local Similarity 88.7%; Pred. No. 4.5e-27;  
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60  
 DB 3 QMTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 62  
 QY 61 SGGSGYGTDFLTITSSLPEDFSATYYCOQANSFPYTFGQGTKEIKR 106  
 DB 63 SGGSGYGTDFLTITSSLPEDFSATYYCOQANSFPYTFGQGTKEIKR 108

RESULT 15  
 ADP22216  
 ID ADP22216 standard; protein; 107 AA.  
 XX  
 AC ADP22216;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX

DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:122.  
 XX  
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;  
 KM antibacterial; antiinflammatory; immunosuppressive; nephrotropic;  
 KM eating-disorder; immunomodulator; antipapillary; antipapillary;  
 KM neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
 KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;  
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
 KM prostatic cancer; immuno-mediated inflammatory disease;  
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
 KM restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
 KM septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.  
 OS  
 XX WO2004050683-A2.  
 XX  
 XX 17-JUN-2004.  
 XX  
 XX 02-DEC-2003; 2003WO-US038281.  
 XX  
 XX 02-DEC-2002; 2002US-0430729P.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 XX  
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;  
 PI Haak-Frendscho M, Rathanaawami P, Pigott C, Liang ML, Lee R;  
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
 XX  
 XX WPI; 2004-480601/45.  
 DR N-PSDB; ADP22215.  
 XX

XX New recombinant human monoclonal antibody that specifically binds to  
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
 PT arthritis.  
 XX  
 PS Example 10; SEQ ID NO 122; 213bp; English.

XX The present invention describes a human monoclonal antibody (1) that  
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
 CC (M1) the level of TNFA in a patient sample, comprising contacting with  
 CC (1), and detecting the level of binding between the antibody and TNFA in  
 CC the sample; (2) a composition comprising the antibody or its functional  
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a  
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
 CC animal in need of treatment for the disease by administering the human  
 CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFA induced  
 CC apoptosis in an animal by selecting an animal in need of treatment for  
 CC TNFA induced apoptosis by administering the human monoclonal antibody of  
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic, eating-  
 CC antibacterial, antiinflammatory, antipapillary, antipapillary, eating-  
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,  
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
 CC as a TNFA antagonist. The antibody (1) is useful in the preparation of as  
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
 CC diseases such as rheumatoid arthritis, glomerulonephritis,  
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
 CC multiple sclerosis. The present sequence represents a human anti-TNFA  
 CC antibody heavy chain variable region, which is used in the  
 CC exemplification of the present invention.

XX Sequence 107 AA;  
 SQ

Query Match 88.7%; Score 487; DB 8; Length 107;  
 Best Local Similarity 89.5%; Pred. No. 5.3e-27;  
 Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60  
 DB 3 QMTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 62  
 QY 61 SGGSGYGTDFLTITSSLPEDFSATYYCOQANSFPYTFGQGTKEIKR 105  
 DB 63 SGGSGYGTDFLTITSSLPEDFSATYYCOQANSFPYTFGQGTKEIKR 107

Search completed: August 30, 2006, 00:41:51  
 Job time : 97.2394 secs



GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: August 30, 2006, 00:32:06 ; Search time 9.95758 Seconds  
(without alignments)  
1024.243 Million cell updates/sec

Title: US-10-027-725A-12

Sequence: 1 ELTQSPSSVSAVGDRTVIT.....QQANSPFYTGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:.\*  
2: PIR1:.\*  
3: PIR2:.\*  
4: PIR3:.\*  
5: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	84.2	117	2	S46376 Ig kappa chain V-J
2	462	84.2	125	2	S40316 Ig kappa chain - h
3	459	83.6	125	2	S40333 Ig kappa chain V-J
4	455	82.9	125	2	S40349 Ig kappa chain V-J
5	454.5	82.8	124	2	S40336 Ig kappa chain V-J
6	454	82.7	120	2	S40368 Ig kappa chain - h
7	451	82.1	128	2	S46372 Ig light chain var
8	451	82.1	131	2	S40352 Ig kappa chain V-J
9	450	82.0	105	2	S36266 Ig lambda chain V
10	447	81.4	127	2	S40367 Ig kappa chain V-J
11	446	81.2	108	2	S19674 Ig kappa chain V r
12	446	81.2	132	2	S38646 Ig kappa chain V r
13	445	81.1	117	2	S46371 Ig kappa chain V-J
14	444	80.9	123	2	S40331 Ig kappa chain - h
15	444	80.9	132	2	S40334 Ig kappa chain - h
16	443	80.7	108	2	B49047 Ig kappa chain V r
17	441	80.3	108	2	S47182 Ig kappa chain - h
18	441	80.3	109	2	S31998 Ig kappa chain - h
19	441	80.3	124	2	S40318 Ig kappa chain V r
20	439.5	80.1	108	2	S30521 Ig kappa chain V r
21	439	80.0	129	2	S40369 Ig kappa chain - h
22	437	79.6	107	2	S36264 Ig lambda chain V
23	435.5	79.3	108	2	S34007 Ig kappa chain V r
24	435	79.2	108	1	K1HUBN Ig kappa chain V-I
25	434.5	79.1	107	2	S36275 Ig lambda chain V
26	434	79.1	108	1	K1HUMS Ig kappa chain V-I
27	434	79.1	108	2	S44122 Ig kappa chain V r
28	433	78.9	117	2	S21527 Ig kappa chain pre
29	432	78.7	108	2	S36283 Ig lambda chain V

30	431.5	78.6	107	2	S47183 Ig kappa chain - h
31	431	78.5	107	2	S36262 Ig lambda chain V
32	428	78.0	107	2	S36269 Ig lambda chain V
33	427	77.8	109	2	S31981 Ig kappa chain - h
34	426.5	77.7	107	1	K1HUMR Ig kappa chain V-I
35	426	77.6	108	2	S36277 Ig lambda chain V
36	426	77.6	109	2	S31979 Ig kappa chain - h
37	426	77.6	110	2	PN0535 Ig kappa chain V r
38	426	77.6	122	2	S40370 Ig kappa chain - h
39	426	77.6	141	2	A49314 Ig kappa chain V-I
40	424	77.2	107	2	I69017 anti-HIV envelope
41	424	77.2	108	1	K1HUMK Ig kappa chain V-I
42	424	77.2	129	1	K1HUMK Ig kappa chain pre
43	423	77.0	108	1	K1HUGL Ig kappa chain V-I
44	423	77.0	108	1	K1HUMU Ig kappa chain V-I
45	423	77.0	126	2	S40335 Ig kappa chain V-J

## ALIGNMENTS

## RESULT 1

S46376 Ig kappa chain V-J region (T33-14) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000

C/Accession: S46376; S38649

R/Benson, C.; Chaetagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination

A/Accession: S46376; MUID:94313975; PMID:8039491

A/Molecule type: mRNA

A/Residues: 1-117 &lt;BEN&gt;

A/Cross-references: UNIPARC:UPI00001165A9; EMBL:Z27177; NID:9415969; PIDN:CAA81701.1; PIR

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/25-99/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 84.2%; Score 462; DB 2; Length 117;

Best Local Similarity 84.9%; Pred. No. 2.2e-32;

Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITCRASQGISWLAAYOHQGRAPKLLIYASSLQGVPSRF 60

Db 12 QMTQSPSSVSAVGDRTVITCRASQDISWLAAYOHQGRAPKLLIYASSLQGVPSRF 71

Qy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSPFYTGQTKVEIKR 106

Db 72 SGSGSGTDFLTISLQPEDFATYCCQANSPFYTGQTKVEIKR 117

## RESULT 2

S40316 Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C/Accession: S40316

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40316

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-125 &lt;KLE&gt;

A/Cross-references: UNIPARC:UPI0000176CAD; EMBL:X72426

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/31-105/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 84.2%; Score 462; DB 2; Length 125;

Best Local Similarity 85.8%; Pred. No. 2.4e-32;





QY 62 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106  
 Db 64 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 108

## RESULT 12

S38646  
 Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S38646  
 R/Benson: C.; Chastagner, P.; Zouali, M.  
 Submitted to the EMBL Data Library, November 1993  
 A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.  
 A/Reference number: S38643  
 A/Accession: S38646  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-132 <BEN>  
 A/Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27172; NID:g415961; PIDD:CAA81697.1; PTC/Suprafamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/40-114/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 132;  
 Best Local Similarity 82.9%; Pred. No. 5.6e-31;  
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISSWLAWYQHOGPKAPKLLIYSASSLSQGVPSRF 61  
 Db 28 IAGSPSSLSASVGDRTVITTCRASQGISSWLAWYQOKPKAPKLLIYASTLSQGVPSRF 87  
 QY 62 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106  
 Db 88 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 132

## RESULT 13

S46371  
 Ig kappa chain V-J region (724-3) - human (fragment)

C/Species: Homo sapiens (man)  
 C/Date: 27-Jan-1995 #sequence\_revision 01-Sep-1995 #text\_change 21-Jan-2000  
 C/Accession: S46371; S38645  
 R/Benson: C.; Chastagner, P.; Zouali, M.  
 EMBL:J. 13, 2951-2962, 1994  
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination  
 A/Reference number: S46369; MUID:94313975; PMID:8039491  
 A/Accession: S46371  
 A/Molecule type: mRNA  
 A/Residues: 1-117 <BEN>  
 A/Cross-references: UNIPARC:UPI00001165A4; EMBL:Z27172; NID:g415959; PIDD:CAA81696.1; PTC/Suprafamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/23-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 445; DB 2; Length 117;  
 Best Local Similarity 78.7%; Pred. No. 6.1e-31;  
 Matches 85; Conservative 14; Mismatches 7; Indels 2; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISSWLAWYQHOGPKAPKLLIYSASSLSQGVPSRF 60  
 Db 10 QMTQSPSTLSASVGDRTVITTCRASRSISTWLAWYQOKPKAPKLLIYKASTLSQGVPSRF 69  
 QY 61 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106  
 Db 70 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 117

## RESULT 14

S40331  
 Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40331  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40331  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-123 <KLE>  
 A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDD:CAA51109.1; PTC/Suprafamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 123;  
 Best Local Similarity 83.8%; Pred. No. 7.8e-31;  
 Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISSWLAWYQHOGPKAPKLLIYSASSLSQGVPSRF 60  
 Db 19 QMTQSPSTLSASVGDRTVITTCRASQGISSWLAWYQOKPKAPKLLIYASTLSQGVPSRF 78  
 QY 61 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 105  
 Db 79 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 123

## RESULT 15

S40334  
 Ig kappa chain - human

C/Species: Homo sapiens (man)  
 C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40334  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40334  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-132 <KLE>  
 A/Cross-references: UNIPARC:UPI0000176CA9; EMBL:X72444  
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 132;  
 Best Local Similarity 80.2%; Pred. No. 8.3e-31;  
 Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISSWLAWYQHOGPKAPKLLIYSASSLSQGVPSRF 60  
 Db 24 QLTQSPSTLSASVGDRTVITTCRASQGISSWLAWYQOKPKAPKLLIYASTLSQGVPSRF 83  
 QY 61 GSGVGTDFSLTISLQFEDSATYCCQANSFPYTFGGGTKEIKR 106  
 Db 84 GSGSGTDFLTLSLQFEDPATYCCQANSFPYTFGGGTKEIKR 129

Search completed: August 30, 2006, 00:42:54  
 Job time : 9.95758 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:29:05 ; Search time 57.8182 Seconds  
(without alignments)

1695.862 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVASVGDVIT.....QANSPFYFGGKTVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	88.0	236	2	O6GMX8 HUMAN
2	444	80.9	236	2	O6GMW1 HUMAN
3	443	80.7	236	2	O6PIH7 HUMAN
4	437	79.6	108	2	O9UL70 HUMAN
5	437	79.6	108	2	O9UL77 HUMAN
6	435	79.2	108	1	KV1V_HUMAN
7	434	79.1	108	1	KV1S_HUMAN
8	434	79.1	108	2	O9UL79 HUMAN
9	429	78.1	236	2	O5O2W4 HUMAN
10	429	78.1	236	2	O6GMX9 HUMAN
11	427	77.8	244	2	O6S2C8 HUMAN
12	426.5	77.7	107	1	KV1D_HUMAN
13	426.5	77.7	107	2	O96S89 HUMAN
14	426.5	77.6	234	2	O7Z473 HUMAN
15	425	77.4	236	2	O7Z3Y4 HUMAN
16	424	77.2	108	1	KV1R_HUMAN
17	424	77.2	129	1	KV1W_HUMAN
18	424	77.0	236	2	O6PIH5 HUMAN
19	423	77.0	108	1	KV1G_HUMAN
20	423	77.0	108	1	KV1H_HUMAN
21	423	77.0	240	2	O6S2C9 HUMAN
22	419	76.3	108	1	KV1P_HUMAN
23	419	76.3	108	1	KV1L_HUMAN
24	419	76.3	189	2	O56917 HUMAN
25	416	75.8	108	1	KV1O_HUMAN
26	416	75.8	236	2	O6GMX0 HUMAN
27	416	75.8	236	2	O6PIH4 HUMAN
28	413	75.2	108	2	KV1B_HUMAN
29	411.5	75.0	107	2	O9UL81 HUMAN
30	410	74.7	108	1	KV1M_HUMAN
31	408	74.3	108	1	KV1E_HUMAN

32	406	74.0	108	1	KV1A_HUMAN	P01593 homo sapien
33	405	73.8	108	1	KV1P_HUMAN	P01608 homo sapien
34	403	73.4	234	2	O5EF66 HUMAN	O5EF66 homo sapien
35	402	73.2	117	1	KV1I_HUMAN	P01601 homo sapien
36	401	73.0	108	1	KV1N_HUMAN	P01606 homo sapien
37	401	73.0	108	1	KV1Y_HUMAN	P80362 homo sapien
38	394	71.8	117	1	KV1J_HUMAN	P01602 homo sapien
39	393	71.6	108	1	KV1C_HUMAN	P01605 homo sapien
40	391	71.2	108	1	KV1K_HUMAN	P01603 homo sapien
41	385	70.1	108	1	KV1Q_HUMAN	P01609 homo sapien
42	385	70.1	129	1	KV1X_HUMAN	P04432 homo sapien
43	383	69.8	108	1	KV5S_MOUSE	P01652 mus musculu
44	382	69.6	108	2	O9UL83 HUMAN	Q9UL83 homo sapien
45	380	69.2	108	1	KV5Q_MOUSE	P01650 mus musculu

## ALIGNMENTS

RESULT 1  
O6GMX8 HUMAN  
ID O6GMX8\_HUMAN PRELIMINARY; prt; 236 AA.  
AC O6GMX8;  
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE ICKC protein.  
GN Name=ICKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Bulik S.W.,  
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonCommercial License  
CC EMBL: BC073764; AAH73764.1; -; mRNA.  
DR SNR; O6GMX8; 24-235.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.



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CC EMBL; BC034141; AAB34141.1; -, mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
DR SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

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Query Match 80.7%; Score 443; DB 2; Length 236;
Best Local Similarity 83.0%; Pred. No. 7.9e-38;
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 ELTQSPSSVSAVGVDRVTITCRASQGISWLAHYQHQPGRAPKLLIYSASSLSQGVPSRF 60
DB 25 QLTQSPSSLSASVGDRTVITCRASQGISWLAHYQKPKGKAPMLLIYAASLTQSGVPSRF 84
QY 61 SGSGGTDFSLTSSLSQFEDSATIYCOQANSFPYTRGGQTKVEIKR 106
DB 85 SGSGGTDFSLTSSLSQFEDSATIYCOQANSFPYTRGGQTKVEIKR 130

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## RESULT 4

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Q9UL70_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92078975; PubMed=1660528; DOI=10.1084/jem.174.6.1639;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
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EMBL; AF035044; AAD56280.1; -, mRNA.
DR PIR; P01607; 1BWM.
DR HSSP; P01607; 1BWM.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.

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DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin domain.
FT NON_TER 1 108
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

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Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.4e-37;
Matches 85; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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QY 1 ELTQSPSSVSAVGVDRVTITCRASQGISWLAHYQHQPGRAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITCRASQGISWLAHYQKPKGKAPMLLIYAASLTQSGVPSRF 62
QY 61 SGSGGTDFSLTSSLSQFEDSATIYCOQANSFPYTRGGQTKVEIKR 106
DB 63 SGSGGTDFSLTSSLSQFEDSATIYCOQANSFPYTRGGQTKVEIKR 108

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## RESULT 5

```

Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92387224; PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Iuzatatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
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EMBL; AF035037; AAD56273.1; -, mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWM.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.

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DR SMART: SM00406; IGV: 1.  
 DR PROSITE: PSS0835; IG LIKE: 1.  
 KW Immunoglobulin domain.  
 FT NON\_TER 1  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16P3 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;  
 Best Local Similarity 81.1%; Pred. No. 1,4e-37;  
 Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISISWLAHYQHOGKAPKLLIYSASSLQGVPSRF 60  
 Db 3 QMTQSPSSLSASVGDRTVITTCRASQGISISWLAHYQHOGKAPKLLIYSASSLQGVPSRF 62  
 Qy 61 SGSGYGTDFSLTITSLQFEDSATYTCQANSFPYFGQTKVEIKR 106  
 Db 63 TSGSGTDFLTITSLQFEDPATYTCQANSYSTSWTFEGTKVEIKR 108

## RESULT 6

KV1V\_HUMAN STANDARD; PRT; 108 AA.  
 ID KV1V\_HUMAN  
 AC P04430;  
 DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.  
 DT 13-AUG-1987, sequence version 1.  
 DT 07-MAR-2006, entry version 39.  
 DE Ig kappa chain V-I region BAN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=66174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;  
 RA Dwyler F.E., O'Connor T.P., Benson M.D.;  
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
 RL Mol. Immunol. 23:73-78(1986).

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 CC PIR: A01878; KIHMBN.

DR HSSP: P04430; 1WTL.  
 DR SMR: P04430; 1-108.  
 DR GO: GO:0005576; C:extracellular region; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07686; V-set; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG LIKE: 1.  
 KW Amyloid; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT CHAIN 1  
 FT 1  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; C03FD944FE96FDD37 CRC64;

Query Match 79.2%; Score 435; DB 1; Length 108;

Best Local Similarity 78.3%; Pred. No. 2.3e-37;  
 Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISISWLAHYQHOGKAPKLLIYSASSLQGVPSRF 60  
 Db 3 QMTQSPSSLSASVGDRTVITTCRASQGISISWLAHYQHOGKAPKLLIYSASSLQGVPSRF 62  
 Qy 61 SGSGYGTDFSLTITSLQFEDSATYTCQANSFPYFGQTKVEIKR 106  
 Db 63 TSGSGTDFLTITSLQFEDPATYTCQANSYSTSWTFEGTKVEIKR 108

## RESULT 7

KV1S\_HUMAN STANDARD; PRT; 108 AA.  
 ID KV1S\_HUMAN  
 AC P01611;  
 DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
 DT 21-JUL-1986, sequence version 1.  
 DT 07-MAR-2006, entry version 40.  
 DE Ig kappa chain V-I region Wes.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=81092279; PubMed=6778806;  
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolyzate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones protein Wes).";  
 RL Hoppe-Seyler's Z. Physik. Chem. 361:1591-1598(1980).  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

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 CC PIR: A01877; KIHWS.  
 DR HSSP: P01611; 2-108.  
 DR SMR: P01611; 2-108.  
 DR GO: GO:0005576; C:extracellular region; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR InterPro: IPR013106; V-set.  
 DR Pfam: PF07686; V-set; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG LIKE: 1.  
 KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT CHAIN 1  
 FT 1  
 FT REGION 1 23  
 FT REGION 24 34  
 FT REGION 35 49  
 FT REGION 50 56  
 FT REGION 57 88  
 FT REGION 89 97  
 FT REGION 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 79.1%; Score 434; DB 1; Length 108;  
 Best Local Similarity 80.2%; Pred. No. 2.9e-37;  
 Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISISWLAHYQHOGKAPKLLIYSASSLQGVPSRF 60



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Db      3 QMTSPSPSVASVGRDRTITTCRASQDISHILANYQQSGAPKLLIYSSASLSENGVPSNF 62
      :::::
Qy      61 SGSGGYGTFSLITLISLQFEDSATYYCOANSFYTFGGQGVKEIKR 106
      |||:::|
Db      63 SGSGSGTEFTLITSLQPEDPATYFCOANSVELTREGGTVTVIKR 108

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## RESULT 8

Q9ULT79\_HUMAN PRELIMINARY; PRT; 108 AA.  
ID OSUTL79 HUMAN  
AC OSUTL79;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
OX NCBI\_TaxId=9606;  
[1]  
NP\_115711.1  
PP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4511;  
RA Wu X., Liu B., Van der Werf P.L., Kalle N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92289816; PubMed=1601042;  
RA Huber C., Klobbeck H.G., Zachau H.G.;  
RT "Ongoing V kappa-J kappa recombination after formation of a productive V kappa-J kappa coding joint."  
RT Eur. J. Immunol. 22:1561-1565(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93170387; PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation".  
RT Eur. J. Immunol. 23:391-397(1993).

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DR EMBL: AF035035; AAD56271.1; -, mRNA.  
DR PIR: S23638; S23638.  
DR PIR: S30521; S30521.  
DR PIR: S34090; S34090.  
DR HSSP: P01607; IBMW.  
DR SMR: Q9UL79; 1-108.  
DR Linkhub; Q9UL79; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR InterPro; IPR013106; V-set.  
DR SMART; SM00409; IG: 1.  
DR SMART; SM00406; IGV: 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.  
FT NON TER 1  
FT NON TER 108  
SQ SEQUENCE 108 AA; 11787 MW; DB5845FF19724FBAE CRC64;

Query Match 79.1%; Score 434; DB 2; Length 108;  
Best local Similarity 81.0%; Pred. No. 2.9e-37;  
Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps

2 LNTPBSVASAGDVTITTCRASGISTSLAWYOHOGKAPKLIIYSASSLSGGVSRRS 6

Dd 4 MTSPLSLASSTDDRNTTISCRMVGQSISSYLAAMQXKRGKAPPELLIAASTLGSVGRSS 63

Qy 62 GSGVGTDPFLTITSLQFEDSATYCCQANSFPYTPGQGTVEIKR 106

Dd 64 GSGSGTDPFTLITSLQSEDPATYCCQYYSFPPTPGQGTVEIKR 108

## RESULT 9

O502W4	HUMAN		
ID	O502W4	PRELIMINARY;	PRT; 236 AA.
AC	O502W4;		
DT	07-JUN-2005,	integrated into UniProtKB/TrEMBL.	
DT	07-JUN-2005,	sequence version 1.	
DT	07-FEB-2006,	entry version 7.	
DE	IGKC protein..		
GN	Name=IGKC;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OC	Homo.		
CX	NCBI_TaxID=9606;		

RP	NICTEOTIDE SEQUENCE.
RK	TSSBTE=gladular pool- thyroid;
RX	MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schler G.D.,
RA	Altshul S.F., Zeeberg B., Butow K.H., Schaefer C.J., Bhat N.K.,
RA	Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
RA	Datchenko L., Marinina K., Farmer A., Rubin C.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulky S.W.,
RA	Vallion D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schnut J., Myers R.M.,
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RL	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]	
RP	NICTEOTIDE SEQUENCE.
RK	TSSBTE=gladular pool- thyroid;
RX	NIH MGC Project;
RA	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC	-----
EMBL	BC095489, AAHS95489.1, - mRNA.
Ensembl	; ENSG00000163245; Homo sapiens.
InterPro	; IPR003599; IG_1.
InterPro	; IPR007110; IG-like.
InterPro	; IPR003597; IG-cl.
InterPro	; IPR003506; IG_mHC.
InterPro	; IPR003596; IG_v.
Pfam	; PF07654; Cl-set; 1.
SMART	; SM00409; IG_1.
SMART	; SM00407; IGC1; 1.
SMART	; SM00406; IGV; 1.
PROSITE	; PS50835; IG_LIKE; 2.
PROSITE	; PS00290; IG_mHC; UNKNOWN_1.
SEQUENCE	236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query March	78.1%	Score 429;	DB 2;	length 236;
Best Local Similarity	79.2%	Pred. No. 2.3e-36;		
Matches 84;	Conservative 11;	Mismatches 11;	Indels 0;	Gaps 0;

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QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLMAYQHOPGKAPKLLIYSASSLQSGVPSRF 60
Db 25 QMTQSPSSLSASVGRDRTITTCRASQGISRLNGLGWQKPGKAPKLLIFALSSLSGVSRRF 84
QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 106
Db 85 SSGSGTDFLTITSLQPEDFATYTCQANSYPRTFPGQGTKEIKR 130

RESULT 10
Q6GMX9_HUMAN PRELIMINARY; PRT; 236 AA.
AC O6GMX9;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE IGC protein.
GN Name=IGC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomihata S., Canninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC073763; AAH73763.1; -, mRNA.
DR SMR: O6GMX9: 23-236
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG.C1.
DR InterPro: IPR003006; IG.MHC.
DR InterPro: IPR003596; IG.V.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGc1; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG LIKE; 2.
DR PROSITE: PS00290; IG.MHC; UNKOWN 1.
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;

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Query Match 78.1%; Score 429; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 2,3e-36;
Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLMAYQHOPGKAPKLLIYSASSLQSGVPSRF 60
Db 25 QMTQSPSSLSASVGRDRTITTCRASQGISRLNGLGWQKPGKAPKLLIFALSSLSGVSRRF 84
QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 106
Db 85 SSGSGTDFLTITSLQPEDFATYTCQANSYPRTFPGQGTKEIKR 130

RESULT 11
Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontemann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).
CC -----
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CC -----
DR EMBL: Y13057; CAA73500.1; -, mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003596; IG.V.
DR InterPro: IPR013106; V-set.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IG; 2.
DR PROSITE: PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17B68338F2BF CRC64;

Query Match 77.8%; Score 427; DB 2; Length 244;
Best Local Similarity 75.5%; Pred. No. 3,9e-36;
Matches 80; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLMAYQHOPGKAPKLLIYSASSLQSGVPSRF 60
Db 139 QMTQSPSSLSASVGRDRTITTCRASQGISRLNGLGWQKPGKAPKLLIFALSSLSGVSRRF 198
QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSFPYTFGQGTKEIKR 106
Db 199 SSGSGTDFLTITSLQPEDFATYTCQANSYPRTFPGQGTKEIKR 244

RESULT 12
KV1D_HUMAN STANDARD; PRT; 107 AA.
AC KV1D_HUMAN;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Ig kappa chain V-1 region CAR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=75075135; PubMed=4216454;  
 RA Mistein C.P., Deveron E.V.;  
 RT "Primary structure of kappa light chain from a human myeloma protein";  
 RL Eur. J. Biochem. 49:377-391(1974).  
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.  
 CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.  
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 CC -----  
 DR PIR; A01864; KIHUAR.  
 DR HSSP; P80362; 1MTL.  
 DR SMR; P01596; 1-107.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003596; Ig V.  
 DR InterPro; IPR013106; V-set.  
 DR Pfam; PF07686; V-set; 1.  
 DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Direct protein sequencing; Glycoprotein; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT CHAIN 1 >107  
 FT CARBOHYD 28  
 FT NON TER 107  
 SQ SEQUENCE 107 AA; 11704 MW; E1BFD0F844C346 CRC64;  
 Query Match 77.7%; Score 426.5; DB 1; Length 107;  
 Best Local Similarity 76.4%; Pred. No. 1.7e-36;  
 Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;  
 QY 1 ELTQSSVSASVGVDRVTTCRASQGISWLMWYOHQPKAPKLLIYSASSLSQGVPSRF 60  
 DB 3 QMTQSPSTLSASVGRVAITCRASQNISSWLMWYQKPKAPKLLIYSASSLSQGVPSRF 62  
 QY 61 SSGSGYTDFTLTISLQPEDSATYTCQANSFPYFGGTKEIKR 106  
 DB 63 SSGSGYTDFTLTISLQPBPAFYTCQQYVTF-FTFGGTKEIKR 107  
 RESULT 13  
 ID Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9;  
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 18.  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain  
 DE variable region (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.B., Shikman A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal monoclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes";

RL J. Immunol. 161:2020-2031(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92387224; PubMed=1516616;  
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;  
 RT "Human monoclonal stritral autoantibodies isolated from thymic B  
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene  
 RT segments associated with the autoimmune repertoire";  
 RL Eur. J. Immunol. 22:2231-2236(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93170387; PubMed=8436174;  
 RA Wagner S.D., Luzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92078875; PubMed=1660528; DOI=10.1084/jem.174.6.1639;  
 RA Manheimer-Lory A., Katz J.B., Pillingner M., Ghossein C., Smith A.,  
 RA Diamond B.;  
 RT "Molecular characteristics of antibodies bearing an anti-DNA-  
 RT associated idiotype";  
 RL J. Exp. Med. 174:1639-1652(1991).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=91243737; PubMed=1903706;  
 RA Blaison G., Kuntz J.L., Pasquall J.L.;  
 RT "Molecular analysis of V kappa III variable regions of polyclonal  
 RT rheumatoid factors during rheumatoid arthritis";  
 RL Eur. J. Immunol. 21:1221-1227(1991).  
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 CC -----  
 DR EMBL; U96396; AAB68785.1; -; mRNA.  
 DR PIR; B49047; B49047.  
 DR PIR; PH0867; PH0867.  
 DR PIR; S16840; S16840.  
 DR PIR; S31977; S31977.  
 DR PIR; S34083; S34083.  
 DR PIR; S34086; S34086.  
 DR HSSP; P01607; 1BMW.  
 DR SMR; Q96SA9; 1-107.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR LinkHub; Q96SA9; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003596; Ig V.  
 DR InterPro; IPR013106; V-set.  
 DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin domain.  
 FT NON TER 1  
 FT NON TER 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;  
 Query Match 77.7%; Score 426.5; DB 2; Length 107;  
 Best Local Similarity 82.1%; Pred. No. 1.7e-36;  
 Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;  
 QY 1 ELTQSSVSASVGVDRVTTCRASQGISWLMWYOHQPKAPKLLIYSASSLSQGVPSRF 60  
 DB 3 QMTQSPSTLSASVGRVITTCRASQISISYLMWYQKPKAPKLLIYAASSLSQGVPSRF 62  
 QY 61 SSGSGYTDFTLTISLQPEDSATYTCQANSFPYFGGTKEIKR 106  
 DB 63 SSGSGYTDFTLTISLQPBPAFYTCQQYS-TLTFGGTKEIKR 107  
 RESULT 14

972473\_HUMAN PRELIMINARY; PRT; 234 AA.  
AC Q72473.1  
DT 01-OCT-2003, integrated version UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 07-FEB-2006, entry version 21.  
DE IGC protein.  
GN Name=IGC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEBLIN=22386257, PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Butler K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Mursina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loughelano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodigues A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywicki M.T., Skalska U., Smallus D.E.,  
RA Scherzer A., Schin J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RG NIH MGC Project;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
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CC -----  
CC EMBL: BC056256; AAH56256.1; -, mRNA.  
CC HSRP: P01834; 1HRZ.  
DR SMR: Q72473.1; 22-234.  
DR Ensemble: ENSG00000163245; Homo sapiens.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-1like.  
DR InterPro: IPR003597; IG\_C1.  
DR InterPro: IPR003066; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR InterPro: IPR013106; V-set.  
DR Pfam: PF07654; C1-set; 1.  
DR SMART: SM00409; IG; 1.  
DR SMART: SM00407; IGC1; 1.  
DR PROSITE: PS00835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN 1.  
DR SEQUENCE 234 AA; 25674 MW; 1A2C259BAM51BC0F CRC64;

DB 84 GSAAGTDPFTLISICLOSEDFATYCCQGYTTYPTFGGTKEIKR 128

RESULT 15  
ID 0723Y4 HUMAN PRELIMINARY; PRT; 236 AA.  
AC 0723Y4;  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DT 07-FEB-2006, entry version 20.  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Struhsberg R., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marnins K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,  
RA Raha S.S., Loughellano N.A., Peters G.J., Aramson R.D., Mullaly S.J.,  
RA Bosak S.A., McNamee P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Morley K.C., Hale S., García A.M., Gay L.J., Hultky S.W.,  
RA Fabry J., Helton E., Kettelman M., Madan A.C., Rodríguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rothergiz A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Ruedigerfeld Y.S.N., Krzywnicki M.I., Skalska U., Smallus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Skeletal Muscle;  
RX Struhsberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
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CC -----  
CC EMBL: BC005332; AAH05332.1; -, mRNA.  
CC HSSP: P01834; 1HE2.  
CC DR Ensembl: ENSG00000163245; Homo sapiens.  
DR DR InterPro: IPR003599; IG.  
DR DR InterPro: IPR007110; IG-like.  
DR DR InterPro: IPR003597; IG-cl.  
DR DR InterPro: IPR003006; IG\_MHC.  
DR DR InterPro: IPR003596; IG\_V.  
DR DR InterPro: IPR013106; V-set.  
DR DR Pfam: PF07654; C1-set; 1.  
DR DR SMART: SM00409; IG; 1.  
DR DR SMART: SM00407; IGcl; 1.  
DR DR SMART: SM00406; IGV; 1.  
DR DR PROSITE: PS50835; IG\_LIKE; 2.  
DR DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
DR DR Hypothetical protein.  
KW SEQUENCE 236 AA; 25702 MW; 75FEFE4ED32084BC6 CRC64;

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0y      2 LTQSPSSVASVGYDRVTTTCRAAQGISMLAWYQHQPCKAPKLLIYSAASSLQSGVSPRFS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      24 MTQSPSSSFASVGYDRVTTTCRAAQGISGLYAWYQKPKGAPQPLLIIYAASTLQSGVSPRFS 83
0y      62 GSGGYGDSLTLSLQFEDSATYYQQANSPFYTGQGGTKVEIKR 106

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Query Match	77.4%	Score 425;	DB 2;	Length 226;
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				Indels 0;
				Gaps 0.

Db 25 OMTQSPSSLSASVGDVTITICRASQDISNYLAWFOQKPGKAPKSLIYGASISLQSGVQSKF 84  
QY 61 SSGGYGTDPSSLTSSIQFEDSATYCCQANSFPYTFGQGTKEIKR 106  
Db 85 SSGSGSTDPFTLTITSSLOPEDFATYCCQYKSPVTFGQGTKEIKR 130

Search completed: August 30, 2006, 00:35:15  
Job time : 57.8182 secs

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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:35:31 ; Search time 14.4545 Seconds  
(without alignments)  
641.891 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGRVITTT.....OQANSPPYFGQTKVEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/prodata/2/1aa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/1aa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/1aa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/1aa/H\_COMB.pep:\*  
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6: /EMC\_Celerra\_SIDS3/prodata/2/1aa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518	94.4	233	2	US-08-812-586-45 Sequence 45, App1
2	518	94.4	233	2	US-09-535-832A-42 Sequence 42, App1
3	475	86.5	236	2	US-09-859-053-30 Sequence 30, App1
4	466	84.9	108	2	US-09-970-262A-8 Sequence 8, App1
5	466	84.9	109	1	US-07-934-373C-3 Sequence 3, App1
6	466	84.9	109	2	US-08-437-642B-3 Sequence 3, App1
7	466	84.9	109	2	US-08-146-206C-3 Sequence 3, App1
8	466	84.9	109	2	US-09-705-686-3 Sequence 3, App1
9	466	84.9	109	2	US-09-705-392A-3 Sequence 3, App1
10	466	84.9	109	2	US-09-705-398-3 Sequence 3, App1
11	466	84.9	109	5	PCT-US93-07832-3 Sequence 3, App1
12	464.5	84.6	109	2	US-09-798-058-4 Sequence 4, App1
13	463	84.3	107	2	US-09-240-274-40 Sequence 40, App1
14	463	84.3	107	1	US-08-848-798-40 Sequence 40, App1
15	460	83.8	107	1	US-08-276-852-104 Sequence 104, App
16	460	83.8	107	1	US-08-899-575-104 Sequence 104, App
17	460	83.8	107	2	US-08-899-575-104 Sequence 104, App
18	460	83.8	107	2	US-09-644-668A-13 Sequence 13, App1
19	460	83.8	107	5	PCT-US95-08743-104 Sequence 104, App
20	460	83.8	108	2	US-08-974-899-3 Sequence 3, App1
21	460	83.8	108	2	US-09-795-798-3 Sequence 3, App1
22	460	83.8	108	2	US-08-908-469-12 Sequence 12, App1
23	459	83.6	128	1	US-08-259-372A-14 Sequence 14, App1
24	459	83.6	128	1	US-08-468-671-14 Sequence 14, App1
25	457	83.2	107	1	US-08-276-852-84 Sequence 84, App1
26	457	83.2	107	1	US-08-899-575-84 Sequence 84, App1

27	457	83.2	107	1	US-08-899-575-84 Sequence 84, App1
28	457	83.2	107	2	US-09-240-274-175 Sequence 175, App
29	457	83.2	107	2	US-09-240-274-176 Sequence 176, App
30	457	83.2	107	2	US-09-848-798-175 Sequence 175, App
31	457	83.2	107	2	US-09-848-798-176 Sequence 176, App
32	457	83.2	107	5	PCT-US95-08743-84 Sequence 84, App1
33	456	83.1	107	2	US-09-848-798-156 Sequence 156, App
34	456	83.1	107	2	US-09-848-798-156 Sequence 156, App
35	456	83.1	109	2	US-09-157-370-3 Sequence 3, App1
36	455	82.9	107	1	US-07-934-373C-18 Sequence 18, App1
37	455	82.9	107	2	US-08-437-642B-18 Sequence 18, App1
38	455	82.9	107	2	US-08-146-206C-18 Sequence 18, App1
39	455	82.9	107	2	US-09-648-067A-14 Sequence 14, App1
40	455	82.9	107	2	US-09-705-686-18 Sequence 18, App1
41	455	82.9	107	2	US-09-705-392A-18 Sequence 18, App1
42	455	82.9	107	2	US-09-705-398-18 Sequence 18, App1
43	455	82.9	107	2	US-09-602-812A-5 Sequence 5, App1
44	455	82.9	107	5	PCT-US93-07832-18 Sequence 18, App1
45	454	82.7	109	2	US-09-025-769B-28 Sequence 28, App1

#### ALIGNMENTS

RESULT 1  
US-08-812-586-45  
; Sequence 45, Application US/08812586  
; Patent No. 6048704  
; GENERAL INFORMATION:  
; APPLICANT: Martin David Tilson  
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
; NUMBER OF INVENTIONS: 61  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/812,586  
; FILING DATE: 07-MAR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/53862-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ. ID NO.: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-812-586-45  
; Query Match 94.4%; Score 518; DB 2; Length 233;  
; Best local similarity 96.2%; Pred. No. 4.3e-41;  
; Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ELTQSPSSVSASVGRVITTTTCRASQGISGLAWYHQPKAKRLTLTYSASSLSQGVPSRF 60  
DB 23 ELTQSPSSVSASVGRVITTTTCRASQGISGLAWYHQPKAKRLTLTYSASSLSQGVPSRF 82

Qy 61 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 106  
Db 83 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 128

RESULT 2  
US-09-535-832A-42  
; Sequence 42, Application US/09535832A  
; Patent No. 6537769  
; GENERAL INFORMATION:  
; APPLICANT: Tilson, Martin David  
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated  
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and  
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof  
; FILE REFERENCE: 53862-A2  
; CURRENT APPLICATION NUMBER: US/09/535, 832A  
; CURRENT FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-535-832A-42

Query Match 94.4%; Score 518; DB 2; Length 233;  
Best Local Similarity 96.2%; Pred. No. 4.3e-41;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPKAPKLLIYASASSLOSQVPSRF 60  
Db 23 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPKAPKLLIYASASSLOSQVPSRF 82  
Qy 61 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 106  
Db 83 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 128

RESULT 3  
US-09-859-053-30  
; Sequence 30, Application US/09859053  
; Patent No. 6803039  
; GENERAL INFORMATION:  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, No. 6803039uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILM AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859, 053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-859-053-30

Query Match 86.5%; Score 475; DB 2; Length 236;  
Best Local Similarity 88.7%; Pred. No. 4.6e-37;  
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPKAPKLLIYASASSLOSQVPSRF 60  
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISRLLAHYQHPKAPKLLIYASASSLOSQVPSRF 84

Qy 61 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 106  
Db 85 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 130

RESULT 4  
US-09-920-262A-8  
; Sequence 8, Application US/09920262A  
; Patent No. 6902734  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David  
; APPLICANT: Knight, David  
; APPLICANT: Scallion, Bernie  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Peritt, David  
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0248  
; CURRENT APPLICATION NUMBER: US/09/920, 262A  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/223, 358  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 60/236, 827  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver 3.1  
; SEQ ID NO 8  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-262A-8

Query Match 84.9%; Score 466; DB 2; Length 108;  
Best Local Similarity 84.9%; Pred. No. 1.4e-36;  
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPKAPKLLIYASASSLOSQVPSRF 60  
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYQHPKAPKLLIYASASSLOSQVPSRF 62  
Qy 61 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 106  
Db 63 SGGSGTDFSLTISLQPEDSATYTCQOANSFPTFGGKTVEIKR 108

RESULT 5  
US-07-934-373C-3  
; Sequence 3, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Prestia  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Minipain (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934, 373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:



APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-3

Query Match 84.9%; Score 466; DB 1; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1,4e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDVVTITTCRASQGISWLMAYOHQPKAPKLLIYASSLQSGVPSRF 60  
Db 3 QMTQSPSSLSASVGDVVTITTCRASQDVSSYLAHYQKPKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSPPYTFGQGTKEIKR 106  
Db 63 SSGSGGTDFLTITSLQPEDFATYYCQYNLSPLYTFGQGTKEIKR 108

RESULT 6  
US-08-437-642B-3  
Sequence 3, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-3

Query Match 84.9%; Score 466; DB 2; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1,4e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDVVTITTCRASQGISWLMAYOHQPKAPKLLIYASSLQSGVPSRF 60  
Db 3 QMTQSPSSLSASVGDVVTITTCRASQDVSSYLAHYQKPKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSPPYTFGQGTKEIKR 106  
Db 63 SSGSGGTDFLTITSLQPEDFATYYCQYNLSPLYTFGQGTKEIKR 108

RESULT 7  
US-08-146-206C-3  
Sequence 3, Application US/08146206C  
Patent No. 6407213  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,206C  
FILING DATE: 17-No. 6407213-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-146-206C-3

Query Match 84.9%; Score 466; DB 2; Length 109;  
Best Local Similarity 84.9%; Pred. No. 1,4e-36;  
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDVVTITTCRASQGISWLMAYOHQPKAPKLLIYASSLQSGVPSRF 60  
Db 3 QMTQSPSSLSASVGDVVTITTCRASQDVSSYLAHYQKPKAPKLLIYASSLQSGVPSRF 62

QY 61 SSGSGYTDPSLTITSLQFEDSATYTCQANSPPYTFGQGTKEIKR 106  
Db 63 SSGSGGTDFLTITSLQPEDFATYYCQYNLSPLYTFGQGTKEIKR 108

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RESULT 8
US-09-705-686-3
: Sequence 3, Application US/09705686
: Patent No. 6639055
: GENERAL INFORMATION:
: APPLICANT: Carter, Paul J.
: Presta, Leonard G.
: TITLE OF INVENTION: Method for Making Humanized Antibodies
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPacIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/705,686
: FILING DATE: 02-NO. 6639055-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/146206
: FILING DATE: 17-NOV-1993
: APPLICATION NUMBER: 07/715272
: FILING DATE: 14-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0709P1D3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-1994
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 109 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3

Query Match      84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,4e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

CY      1 ELTQSPSSVASVGRVITTCASGISTSLWAWQHQGKAPKLIYASASISQGVPERF 60
      : :::::::::::::::::::::
DB      3 QMTQSPSSISASVGRVITTCASQDVSSYLAWYQKQKAPKLIYASASISLSSGVPSRF 62
      : :::::::::::::::::::::
CY      61 SSGSGGTDFSLTISLQFEDSATYVCCQANSFPYFGQGTKEIKR 106
      : :::::::::::::::::::::
DB      63 SSGSGGTDFSLTISLQPEDFATYVCCQYNLSLPYFGQGTKEIKR 108
      : :::::::::::::::::::::

RESULT 9
US-09-705-392A-3
: Sequence 3, Application US/09705392A
: Patent No. 6719971
: GENERAL INFORMATION:
: APPLICANT: Carter, Paul J.
: Presta, Leonard G.
: TITLE OF INVENTION: Method for Making Humanized Antibodies
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco

```

STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpacin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705.392A  
FILING DATE: 02-NO. 6719971-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/POCKET NUMBER: P0709PId1 REVISED  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-392A-3

RESULT 10  
 US-09-705-398-3  
 ; Sequence 3, Application US/09705398  
 ; Patent No. 6800738  
 ; GENERAL INFORMATION:  
 APPLICANT: Carter, Paul J.  
           Presta, Leonard G.  
 TITLE OF INVENTION: Method for Making Humanized Antibodies  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
     ADDRESSEE: Genentech, Inc.  
     STREET: 1 DNA Way  
     CITY: South San Francisco  
     STATE: California  
     COUNTRY: USA  
     ZIP: 94080  
 COMPUTER READABLE FORM:  
     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
     COMPUTER: IBM PC compatible  
     OPERATING SYSTEM: PC-DOS/MS-DOS  
     SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
     APPLICATION NUMBER: US/09/705,398  
     FILING DATE: 02-No. 6800738-2000  
     CLASSIFICATION: <Unknown>  
     PRIOR APPLICATION NUMBER: 08/146206  
     FILING DATE: 17-NOV-1993

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; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-3

Query Match      84.9%; Score 466; DB 5; Length 109;
Best Local Similarity 84.9%; Pred. No. 1,4e-36;
Matches          90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy
1 ELTQSPSSVASVGDRTITTCRASOGISWLAWOHOPGAPKLLIYSASSLSQGVPSRF 60
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db
3 QMTQSPSSLASVGDRTITTCRASQDVSVTLAWYQQKPKRAPKLLIYAASSLSQGVPSRF 62
|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

61 SSGSGYGFDFSLTISSLQPEDSATYYCOQANSFPPTFGCGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 SSGSGGTFDTLTITSLQPEDFATYYCQQYNLSPTFFQGTRKEIKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-798-058-4
; Sequence 4, Application US/09798058
; Patent No. 6946546
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Wilton, Alison Jane
; APPLICANT: Smith, Stephen
; TITLE OF INVENTION: Human antibodies against eotaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-058-4

Query Match      84.6%; Score 464.5; DB 2; Length 109;
Best Local Similarity 86.0%; Pred. No. 2e-36;
Matches          92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy
1 ELTQSPSSVASVGDRTITTCRASOGISWLAWOHOPGAPKLLIYSASSLSQGVPSRF 60
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db
3 QMTQSPSSVASVGDRTITTCRASQDISSWLAWOHQKRPKAPKLLIYAASSLSQGVPSRF 62
|||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy
61 SSGSYGTDFSLTISSLQPEDSATYYCOQANSFP-YTGCGTKVEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db
63 SSGSGGTFDTLTITSLQPEDFATYYCQQASSFSPTFGGTRLEIKR 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-240-274-40
; Sequence 40, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROMETINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 30, 2006, 00:43:12 ; Search time 60.7091 Seconds  
(without alignments)  
808.788 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSPFTYGQGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	4	US-10-027-725A-12
2	499	90.9	107	6	US-11-051-453-4
3	499	90.9	129	6	US-11-051-453-43
4	493	89.8	107	5	US-10-891-658-80
5	491	89.4	107	5	US-10-727-155-312
6	491	89.4	129	5	US-10-901-901-20
7	490	89.3	107	6	US-11-051-453-32
8	489	89.1	129	6	US-11-051-453-46
9	488	88.9	108	5	US-10-910-901-12
10	488	88.9	108	5	US-10-938-353-109
11	487	88.7	107	5	US-10-727-155-122
12	486	88.5	108	5	US-10-938-353-117
13	485	88.3	107	5	US-10-982-359-67
14	484	88.2	123	4	US-10-693-629-66
15	483	88.0	129	5	US-10-910-901-19
16	482	87.8	107	4	US-10-309-762-159
17	482	87.8	155	6	US-11-131-648-14
18	482	87.8	155	6	US-11-131-648-37
19	481	87.6	107	4	US-10-232-088-105
20	481	87.6	129	5	US-10-910-901-17
21	479	87.2	107	4	US-10-309-762-62
22	479	87.2	107	4	US-10-309-762-164
23	478	87.1	107	4	US-10-309-762-61
24	478	87.1	107	4	US-10-309-762-64
25	478	87.1	244	3	US-09-880-748-1881
26	478	87.1	244	4	US-10-293-418-1881
27	478	87.1	244	6	US-11-054-515-1881

28	478	87.1	244	6	US-11-266-444-1881	Sequence 1881, Ap
29	477	86.9	107	5	US-10-638-265-76	Sequence 76, Appl
30	477	86.9	107	5	US-10-893-576-177	Sequence 177, Appl
31	477	86.9	107	5	US-10-956-008-76	Sequence 76, Appl
32	477	86.9	129	5	US-10-893-576-24	Sequence 24, Appl
33	477	86.9	212	5	US-10-513-725-7	Sequence 7, Appl1
34	475	86.5	236	3	US-09-859-053-30	Sequence 30, Appl
35	475	86.5	236	4	US-10-800-250-30	Sequence 30, Appl
36	475	86.5	236	4	US-10-625-105-30	Sequence 30, Appl
37	474	86.3	107	4	US-10-041-860-43	Sequence 43, Appl
38	474	86.3	107	4	US-10-041-860-218	Sequence 218, Appl
39	474	86.3	107	4	US-10-665-383-64	Sequence 64, Appl
40	474	86.3	236	5	US-10-910-901-16	Sequence 16, Appl
41	473.5	86.2	106	4	US-10-309-762-84	Sequence 84, Appl
42	472	86.0	107	4	US-10-309-762-60	Sequence 60, Appl
43	472	86.0	107	4	US-10-309-762-63	Sequence 63, Appl
44	471	85.8	236	5	US-10-910-901-4	Sequence 4, Appl1
45	468.5	85.3	108	4	US-10-041-860-357	Sequence 357, Appl

#### ALIGNMENTS

```
RESULT 1
US-10-027-725A-12
; Sequence 12, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof.
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-12

Query Match      100.0%; Score 549; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPKAPRLIYASLSQGVPSRF 60
      |||
DB      1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPKAPRLIYASLSQGVPSRF 60
      |||

QY      61 SSGGYTDFSLTISLQFEDSATYYCOANSPFTYGQGTKEIKR 106
      |||
DB      61 SSGGYTDFSLTISLQFEDSATYYCOANSPFTYGQGTKEIKR 106
      |||

RESULT 2
US-11-051-453-4
; Sequence 4, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
```

```
FILE REFERENCE: MJ1-001
CURRENT APPLICATION NUMBER: US/11/051,453
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,357
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 60/613,854
PRIOR FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-453-4
```

```
Query Match 90.9%; Score 499; DB 6; Length 107;
Best Local Similarity 91.4%; Pred. No. 3.8e-36;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTITSLQFEDSATYTCQANSFPYTFGGTKVEIK 105
Db 63 SSGSGGTDFLTITSLQPEDPATYTCQANSFPWTFGGTKVEIK 107
```

## RESULT 3

```
US-11-051-453-43
Sequence 43, Application US/11051453
Publication No. US20050287150A1
GENERAL INFORMATION:
APPLICANT: AMBROSINO, DONNA
APPLICANT: BABCOCK, GREGORY J.
APPLICANT: BROERING, THERESA
APPLICANT: GRAZIANO, ROBERT
APPLICANT: HERNANDEZ, HECTOR JAVIER
APPLICANT: LOWY, ISRAEL
APPLICANT: MANDELL, ROBERT
APPLICANT: MOHRINE, DEBORAH
APPLICANT: THOMAS, JR., WILLIAM D.
APPLICANT: ZHANG, HUI-FEN
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
FILE REFERENCE: MJ1-001
CURRENT APPLICATION NUMBER: US/11/051,453
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,357
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 60/613,854
PRIOR FILING DATE: 2004-09-28
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 43
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-11-051-453-43
```

```
Query Match 90.9%; Score 499; DB 6; Length 129;
Best Local Similarity 91.4%; Pred. No. 4.6e-36;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 25 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGYGTDFSLTITSLQFEDSATYTCQANSFPYTFGGTKVEIK 105
Db 85 SSGSGGTDFLTITSLQPEDPATYTCQANSFPWTFGGTKVEIK 129
```

## RESULT 4

```
US-10-891-658-80
Sequence 80, Application US/10891658
Publication No. US20050074821A1
GENERAL INFORMATION:
APPLICANT: Kennech, Wild
APPLICANT: Treanor, James
APPLICANT: Huang, Haichun
APPLICANT: Inoue, Heather
APPLICANT: Zhang, Tie J.
APPLICANT: Martin, Frank
TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
FILE REFERENCE: 02-1240
CURRENT APPLICATION NUMBER: US/10/891,658
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/487,431
PRIOR FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn version 3.0
SEQ ID NO 80
LENGTH: 107
TYPE: PRT
ORGANISM: homo sapien
US-10-891-658-80
```

```
Query Match 89.8%; Score 493; DB 5; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.3e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTITSLQFEDSATYTCQANSFPYTFGGTKVEIK 105
Db 63 SSGSGGTDFLTITSLQPEDPATYTCQANSFPWTFGGTKVEIK 107
```

## RESULT 5

```
US-10-727-155-312
Sequence 312, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Weina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchio
APPLICANT: Raffaella Faggioli
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 312
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-312
```

Query Match 89.4%; Score 491; DB 5; Length 107;  
Best Local Similarity 90.5%; Pred. No. 1.9e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLMAYQHOPKAPKLLIYASASSLQSGVPSRF 60  
DB 3 QMTQSPSSVASVAGDVTITTCRASQGISWLMAYQKPKAPKLLIYASASSLQSGVPSRF 62  
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105  
DB 63 SSGSGGTDFLTITSSIQPEDFATYYCOQANSFPWTGGGTKEIK 107

## RESULT 6

US-10-910-901-20  
Sequence 20, Application US/10910901  
Publication No. US2005054019A1  
GENERAL INFORMATION:  
APPLICANT: MICHAUD, NEIL R., et al.  
TITLE OF INVENTION: ANTIBODIES TO C-MET  
FILE REFERENCE: ABX-PF5  
CURRENT APPLICATION NUMBER: US/10/910,901  
PRIOR FILING DATE: 2004-08-03  
PRIOR APPLICATION NUMBER: US 60/492,432  
PRIOR FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 20  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-910-901-20

Query Match 89.4%; Score 491; DB 5; Length 129;  
Best Local Similarity 90.5%; Pred. No. 2.3e-35;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLMAYQHOPKAPKLLIYASASSLQSGVPSRF 60  
DB 25 QMTQSPSSVASVAGDVTITTCRASQGISWLMAYQKPKAPKLLIYASASSLQSGVPSRF 84  
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105  
DB 85 SSGSGGTDFLTITSSIQPEDFATYYCOQANSFPWTGGGTKEIK 129

## RESULT 7

US-11-051-453-32  
Sequence 32, Application US/11051453  
Publication No. US20050287150A1  
GENERAL INFORMATION:  
APPLICANT: AMBROSINO, DONNA  
APPLICANT: BABCOCK, GREGORY J.  
APPLICANT: BROERING, THERESA  
APPLICANT: GRAZIANO, ROBERT  
APPLICANT: HERNANDEZ, HECTOR JAVIER  
APPLICANT: LOWY, ISRAEL  
APPLICANT: MANDELL, ROBERT  
APPLICANT: MOLRINE, DEBORAH  
APPLICANT: THOMAS, JR., WILLIAM D.  
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: MJ1-001  
CURRENT APPLICATION NUMBER: US/11/051,453  
PRIOR FILING DATE: 2005-02-04  
PRIOR APPLICATION NUMBER: 60/542,357  
PRIOR FILING DATE: 2004-02-06  
PRIOR APPLICATION NUMBER: 60/613,854  
PRIOR FILING DATE: 2004-09-28  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: PatentIn Ver. 3.3

SEQ ID NO 32  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-051-453-32

Query Match 89.3%; Score 490; DB 6; Length 107;  
Best Local Similarity 89.5%; Pred. No. 2.3e-35;  
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLMAYQHOPKAPKLLIYASASSLQSGVPSRF 60  
DB 3 QMTQSPSSVASVAGDVTITTCRASQGISWLMAYQKPKAPKLLIYASASSLQSGVPSRF 62  
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105  
DB 63 SSGSGGTDFLTITSSIQPEDFATYYCOQANSFPWTGGGTKEIK 107

## RESULT 8

US-11-051-453-46  
Sequence 46, Application US/11051453  
Publication No. US20050287150A1  
GENERAL INFORMATION:  
APPLICANT: AMBROSINO, DONNA  
APPLICANT: BABCOCK, GREGORY J.  
APPLICANT: BROERING, THERESA  
APPLICANT: GRAZIANO, ROBERT  
APPLICANT: HERNANDEZ, HECTOR JAVIER  
APPLICANT: LOWY, ISRAEL  
APPLICANT: MANDELL, ROBERT  
APPLICANT: MOLRINE, DEBORAH  
APPLICANT: THOMAS, JR., WILLIAM D.  
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: MJ1-001  
CURRENT APPLICATION NUMBER: US/11/051,453  
PRIOR FILING DATE: 2005-02-04  
PRIOR APPLICATION NUMBER: 60/542,357  
PRIOR FILING DATE: 2004-02-06  
PRIOR APPLICATION NUMBER: 60/613,854  
PRIOR FILING DATE: 2004-09-28  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 46  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-051-453-46

Query Match 89.3%; Score 490; DB 6; Length 129;  
Best Local Similarity 89.5%; Pred. No. 2.8e-35;  
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVAGDVTITTCRASQGISWLMAYQHOPKAPKLLIYASASSLQSGVPSRF 60  
DB 25 QMTQSPSSVASVAGDVTITTCRASQGISWLMAYQKPKAPKLLIYASASSLQSGVPSRF 84  
QY 61 SSGSGYTDPSLTITSSIQFEDSATYYCOQANSFPYTFGGGTKEIK 105  
DB 85 SSGSGGTDFLTITSSIQPEDFATYYCOQANSFPWTGGGTKEIK 129

## RESULT 9

US-10-910-901-12  
Sequence 12, Application US/10910901  
Publication No. US2005054019A1  
GENERAL INFORMATION:  
APPLICANT: MICHAUD, NEIL R., et al.  
TITLE OF INVENTION: ANTIBODIES TO C-MET  
FILE REFERENCE: ABX-PF5  
CURRENT APPLICATION NUMBER: US/10/910,901

```

; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 12
; LENGTH: 236
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-910-901-12
```

```

Query Match      89.1%; Score 489; DB 5; Length 236;
Best Local Similarity 89.6%; Pred. No. 6.2e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      25 QMTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQOKPGKAPKLLIYAASSLSQGVPSRF 84
```

```
QY      61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      85 SSGSGGTDFTLTITSSLOPEDFATYTCQOANSFPITFGGTKEIKR 130
```

```

RESULT 10
US-10-938-353-109
; Sequence 109, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FREDSCHO, MARY
; APPLICANT: KELLERMANN, STRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 109
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-938-353-109
```

```

Query Match      88.9%; Score 488; DB 5; Length 108;
Best Local Similarity 88.7%; Pred. No. 3.5e-35;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      3 QMTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQOKPGKAPKLLIYAASSLSQGVPSRF 62
```

```
QY      61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      63 SSGSGGTDFTLTITSSLOPEDFATYTCQOANSFPITFGGTKEIKR 108
```

```

RESULT 11
US-10-727-155-122
; Sequence 122, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foorad
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
```

```

Query Match      88.5%; Score 486; DB 5; Length 108;
Best Local Similarity 89.6%; Pred. No. 5.3e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      3 QMTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQOKPGKAPKLLIYAASSLSQGVPSRF 62
```

```
QY      61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      63 SSGSGGTDFTLTITSSLOPEDFATYTCQOANSFPITFGGTKEIKR 108
```

```

; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Fredscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchio
; APPLICANT: Rafeella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Ojaouan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: FACTOR AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 107
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-727-155-122
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Query Match      88.7%; Score 487; DB 5; Length 107;
Best Local Similarity 89.5%; Pred. No. 4.3e-35;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
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QY      1 ELTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      3 QMTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQOKPGKAPKLLIYAASSLSQGVPSRF 62
```

```
QY      61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 105
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      63 SSGSGGTDFTLTITSSLOPEDFATYTCQOANSFPITFGGTKEIKR 107
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RESULT 12
US-10-938-353-117
; Sequence 117, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FREDSCHO, MARY
; APPLICANT: KELLERMANN, STRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 117
; LENGTH: 108
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-938-353-117
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Query Match      88.5%; Score 486; DB 5; Length 108;
Best Local Similarity 89.6%; Pred. No. 5.3e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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QY      1 ELTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB      3 QMTQSPSSVSAASVGDRTVITTCRASQGISSWLAWYQOKPGKAPKLLIYAASSLSQGVPSRF 62
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QY      61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      63 SSGSGGTDFTLTITSSLOPEDFATYTCQOANSFPITFGGTKEIKR 108
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QY      61 SSGSGYGFDSLTITSSLOFEDSATYTCQOANSFPYTFGQGTKEIKR 106
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Db 63 SSGSGTDFLTITSSLPEDFATYYCOQANSFPLTGGTKVEIKR 108

## RESULT 13

US-10-982-359-67  
; Sequence 67, Application US/10982359  
; Publication No. US20050112694A1  
; GENERAL INFORMATION:  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Zhou, Hongxing  
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR  
; FILE REFERENCE: 3492-A  
; CURRENT APPLICATION NUMBER: US/10/982,359  
; PRIOR FILING DATE: 2004-11-04  
; PRIOR APPLICATION NUMBER: 60/518,166  
; PRIOR FILING DATE: 2003-11-07  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 67  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: 63 light chain variable region  
US-10-982-359-67

Query Match 88.3%; Score 485; DB 5; Length 107;  
Best Local Similarity 88.6%; Pred. No. 6,4e-35;  
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQGVPSRF 60  
Db 3 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQGVPSRF 62  
Qy 61 SSGSGTDFSLTITSSLPEDSATYYCOQANSFPYTGQTKVEIK 105  
Db 63 SSGSGTDFLTITSSLPEDFATYYCOQANSFPFTGGTKVDIK 107

## RESULT 14

US-10-693-629-66  
; Sequence 66, Application US/10693629  
; Publication No. US20040120948A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; APPLICANT: MIKAYAMA, Toshitumi  
; APPLICANT: YOSHIDA, Hitoshi  
; APPLICANT: FORCE, Walker, R.  
; APPLICANT: CHEN, Kingjie  
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 021286-0306473  
; CURRENT APPLICATION NUMBER: US/10/693,629  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: PCT/US01/13672  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US09/844,684  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: JP2001/142482  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: JP2001/310535  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US10/040,244  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-693-629-66

Query Match 88.2%; Score 484; DB 4; Length 223;  
Best Local Similarity 87.7%; Pred. No. 1.6e-34;  
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQGVPSRF 60  
Db 25 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQGVPSRF 84  
Qy 61 SSGSGTDFSLTITSSLPEDSATYYCOQANSFPYTGQTKVEIKR 106  
Db 85 SSGSGTDFLTITSSLPEDFATYYCOQANSFPFTGGTKVEIKR 130

## RESULT 15

US-10-910-901-19  
; Sequence 19, Application US/10910901  
; Publication No. US20050054019A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAUD, NEIL R., et al.  
; TITLE OF INVENTION: ANTIBODIES TO C-MET  
; FILE REFERENCE: ABX-PFS  
; CURRENT APPLICATION NUMBER: US/10/910,901  
; PRIOR FILING DATE: 2004-08-03  
; PRIOR APPLICATION NUMBER: US 60/492,432  
; PRIOR FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 19  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-910-901-19

Query Match 88.0%; Score 483; DB 5; Length 129;  
Best Local Similarity 88.6%; Pred. No. 1.2e-34;  
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQGVPSRF 60  
Db 25 QMTQSPSSVSASVGDVVTITTCRASQGISWLAHYQHOPGKAPKLLIYSASLSQGVPSRF 84  
Qy 61 SSGSGTDFSLTITSSLPEDSATYYCOQANSFPYTGQTKVEIK 105  
Db 85 SSGSGTDFLTITSSLPEDFATYYCOQANSFPFTGGTKVDIK 129

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Job time : 60.7091 secs

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Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2006, 00:44:32 ; Search time 12.5273 Seconds  
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578.960 Million cell updates/sec

Title: US-10-027-725a-12

Perfect score: 549  
Sequence: 1 ELTQSPSSVSASVGDVVTIT.....QQANSPFYTGQGTKEIKR 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

#### Database :

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2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US06\_NEW\_PUB.pdp:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_NEW\_PUB.pdp:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	88.9	108	7	US-11-375-221-109 Sequence 109, App
2	486	88.5	108	7	US-11-375-221-117 Sequence 117, App
3	484	88.2	108	6	US-10-981-300-27 Sequence 27, App1
4	484	88.2	155	6	US-10-981-300-2 Sequence 2, App11
5	482	87.8	234	6	US-10-511-436A-92 Sequence 92, App1
6	481	87.6	107	7	US-11-211-917-105 Sequence 105, App1
7	476	86.7	106	6	US-10-981-300-26 Sequence 26, App1
8	468	85.2	234	7	US-11-211-917-24 Sequence 24, App1
9	466	84.9	234	7	US-11-211-917-48 Sequence 48, App1
10	463	84.3	107	7	US-11-211-917-20 Sequence 20, App1
11	463	84.3	107	7	US-11-328-483-40 Sequence 40, App1
12	461	84.0	107	7	US-11-211-917-44 Sequence 44, App1
13	460	83.8	108	7	US-11-254-182-27 Sequence 27, App1
14	460	83.8	108	7	US-11-219-121-23 Sequence 23, App1
15	460	83.8	108	7	US-11-106-762-19 Sequence 19, App1
16	460	83.8	108	7	US-11-228-281-3 Sequence 3, App11
17	460	83.8	108	7	US-11-136-917A-11 Sequence 11, App1
18	460	83.8	214	7	US-11-219-121-27 Sequence 27, App1
19	459	83.6	236	7	US-11-375-221-20 Sequence 20, App1
20	457	83.2	107	7	US-11-328-483-175 Sequence 175, App1
21	457	83.2	107	7	US-11-328-483-176 Sequence 176, App1
22	457	83.2	291	7	US-11-154-103-10 Sequence 10, App1
23	456	83.1	107	7	US-11-328-483-156 Sequence 156, App1
24	456	83.1	108	6	US-10-981-300-21 Sequence 21, App1
25	455	82.9	107	7	US-11-254-182-5 Sequence 5, App11

26	455	82.9	107	7	US-11-295-229-5 Sequence 5, App11
27	455	82.9	107	7	US-11-154-091-5 Sequence 5, App11
28	455	82.9	108	7	US-11-370-301-21 Sequence 21, App1
29	455	82.9	108	7	US-11-370-301-21 Sequence 21, App1
30	454	82.7	107	7	US-11-145-131A-26 Sequence 26, App1
31	454	82.7	109	7	US-11-504-986-14 Sequence 14, App1
32	453	82.5	106	7	US-11-337-300-41 Sequence 41, App1
33	453	82.5	243	7	US-11-337-300-47 Sequence 47, App1
34	453	82.5	244	7	US-11-117-786B-17 Sequence 17, App1
35	453	82.5	244	7	US-11-117-786B-19 Sequence 19, App1
36	453	82.5	245	7	US-11-337-300-51 Sequence 51, App1
37	453	82.5	245	7	US-11-337-300-53 Sequence 53, App1
38	453	82.5	245	7	US-11-337-300-59 Sequence 59, App1
39	453	82.5	245	7	US-11-337-300-63 Sequence 63, App1
40	453	82.5	247	7	US-11-337-300-57 Sequence 57, App1
41	453	82.5	247	7	US-11-337-300-96 Sequence 96, App1
42	453	82.5	248	7	US-11-337-300-61 Sequence 61, App1
43	453	82.5	249	7	US-11-337-300-49 Sequence 49, App1
44	453	82.5	249	7	US-11-337-300-67 Sequence 67, App1
45	453	82.5	249	7	US-11-337-300-69 Sequence 69, App1

#### ALIGNMENTS

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RESULT 1
US-11-375-221-109
; Sequence 109, Application US/11375221
; Publication No. US20060153850A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENSCH, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PE4
; CURRENT APPLICATION NUMBER: US/11/375,221
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US/10/938,353
; PRIOR FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 109
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-375-221-109
Query Match 88.9%; Score 488; DB 7; Length 108;
Best Local Similarity 88.7%; Pred. No. 4.4e-38;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDVVTITTCRASQGISWLAHYOHQPGKAPLLLYASASSLOSQVPSRF 60
DB 3 QMOWSSVSASVGDVVTITTCRASQGISWLAHYQKPGKAPLLLYASASSLOSQVPSRF 62
QY 61 SSGSGTDFSLTITSSLOPEDSATYTYCOQANSFPYTGQGTKEIKR 106
DB 63 SSGSGTDFLTITSSLOPEDFATYTYCOQANSFPFTGPGTKVIDIKR 108
RESULT 2
US-11-375-221-117
; Sequence 117, Application US/11375221
; Publication No. US20060153850A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
```

```

; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FREDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PP4
; CURRENT APPLICATION NUMBER: US/11/375,221
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US/10/938,353
; PRIOR FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-375-221-117
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Query Match      88.5%; Score 486; DB 7; Length 108;
Best Local Similarity 89.6%; Pred. No. 6,7e-38;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 62
Qy 61 SSGSGYTDFTLTISLQPEDSATYTCQOANSFPYTFGGGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGYTDFTLTISLQPEDPATYTCQOANSFPYTFGGGTVEIKR 108
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RESULT 3
US-10-981-300-27
; Sequence 27, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 108
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-981-300-27
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```

Query Match      88.2%; Score 484; DB 6; Length 108;
Best Local Similarity 89.6%; Pred. No. 1e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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```

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 62
Qy 61 SSGSGYTDFTLTISLQPEDSATYTCQOANSFPYTFGGGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGYTDFTLTISLQPEDPATYTCQOANSFPYTFGGGTVEIKR 108
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RESULT 4
US-10-981-300-2
; Sequence 2, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
```

```

; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 155
; TYPE: PRT
; ORGANISM: homo sapien
US-10-981-300-2
```

```

Query Match      88.2%; Score 484; DB 6; Length 155;
Best Local Similarity 89.6%; Pred. No. 1.5e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 60
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Db 3 QMTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 62
Qy 61 SSGSGYTDFTLTISLQPEDSATYTCQOANSFPYTFGGGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGYTDFTLTISLQPEDPATYTCQOANSFPYTFGGGTVEIKR 108
```

```

RESULT 5
US-10-511-436A-92
; Sequence 92, Application US/10511436A
; Publication No. US20060148039A1
; GENERAL INFORMATION:
; APPLICANT: KOBAYASHI, KAZUO
; APPLICANT: KITAGAWA, YOSHINORI
; APPLICANT: KOMEDA, TOSHIHIRO
; APPLICANT: KAWASHIMA, NAGAO
; APPLICANT: JIGAMI, YOSHIFUMI
; APPLICANT: CHIBA, YASUNORI
; TITLE OF INVENTION: METHYLOTROPH PRODUCING MAMMALIAN TYPE SUGAR CHAIN
; FILE REFERENCE: 081356-0224
; CURRENT APPLICATION NUMBER: US/10/511,436A
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: PCT/JP03/05464
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: JP 2002-127677
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 92
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-436A-92
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```

Query Match      87.8%; Score 482; DB 6; Length 234;
Best Local Similarity 89.6%; Pred. No. 3.4e-37;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQSPSSVSAVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASSLQSGVPSRF 82
Qy 61 SSGSGYTDFTLTISLQPEDSATYTCQOANSFPYTFGGGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGYTDFTLTISLQPEDPATYTCQOANSFPYTFGGGTVEIKR 128
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RESULT 6
US-11-211-917-105
; Sequence 105, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
```

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; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-105

Query Match      87.6%; Score 481; DB 7; Length 107;
Best Local Similarity 89.5%; Pred. No. 1.9e-37;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTITSLQFEDSATYYCOQANSFPYTFGGGTKEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGTDFLTITSLQPEDFATYYCOQANSFPLTRGGGTKEIKR 107
```

```

RESULT 7
US-10-981-300-26
; Sequence 26, Application US/10981300
; Publication No. US20060093559A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 106
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-981-300-26
```

```

Query Match      86.7%; Score 476; DB 6; Length 106;
Best Local Similarity 89.6%; Pred. No. 5.5e-37;
Matches 95; Conservative 5; Mismatches 4; Indels 2; Gaps 1;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTITSLQFEDSATYYCOQANSFPYTFGGGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGTDFLTITSLQPEDFATYYCOQANSF--TRGGGTKEIKR 106
```

```

RESULT 8
US-11-211-917-24
; Sequence 24, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
```

```

; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-24

Query Match      85.2%; Score 468; DB 7; Length 234;
Best Local Similarity 86.8%; Pred. No. 6.6e-36;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 82
QY 61 SSGSGYGTDFSLTITSLQFEDSATYYCOQANSFPYTFGGGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTDFLTITSLQPEDFATYYCOQANSFPLTRGGGTKEIKR 128
```

```

RESULT 9
US-11-211-917-48
; Sequence 48, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-48
```

```

Query Match      84.9%; Score 466; DB 7; Length 234;
Best Local Similarity 85.8%; Pred. No. 1e-35;
Matches 91; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYSTSTLQSGVPSRF 82
QY 61 SSGSGYGTDFSLTITSLQFEDSATYYCOQANSFPYTFGGGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SSGSGGTDFLTITSLQPEDFATYYCOQANSIFPLTRGGGTKEIKR 128
```

```

RESULT 10
US-11-211-917-20
```

```
; Sequence 20, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-20
```

```
Query Match      84.3%; Score 463; DB 7; Length 107;
Best Local Similarity 86.7%; Pred. No. 8.6e-36;
Matches 91; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSVASVGDVVTITTCRASQGISISWLAHYQHOPGKAPKLLIYASASSLOGSVPSRF 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      3 QMTQSPSSVASVGDVVTITTCRASQGISISWLAHYQHOPGKAPKLLIYASASSLOGSVPSRF 62

QY      61 SSGSGYTDPSLTISLQPEDSATYYCOQANSFPTFGGKVEIK 105
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      63 SSGSGYTDPSLTISLQPEDPATYYCOQTDSPFLFGGKVEIK 107
```

```
RESULT 11
US-11-328-483-40
; Sequence 40, Application US/11328483
; Publication No. US20060177440A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/328,483
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 109
US-11-328-483-40
```

```
Query Match      84.3%; Score 463; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 8.6e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSVASVGDVVTITTCRASQGISISWLAHYQHOPGKAPKLLIYASASSLOGSVPSRF 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      2 ELTQSPSSIASVGDVVTITTCRASQGISISWLAHYQHOPGKAPKLLIYASASSLOGSVPSRF 61
```

```
QY      61 SSGSGYTDPSLTISLQPEDSATYYCOQANSFPTFGGKVEIK 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      62 SSGSGYTDPSLTISLQPEDPATYYCOQANSFPTFGGKVEIK 107
```

```
RESULT 12
US-11-211-917-44
; Sequence 44, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-44
```

```
Query Match      84.0%; Score 461; DB 7; Length 107;
Best Local Similarity 85.7%; Pred. No. 1.3e-35;
Matches 90; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
```

```
QY      1 ELTQSPSSVASVGDVVTITTCRASQGISISWLAHYQHOPGKAPKLLIYASASSLOGSVPSRF 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      3 QMTQSPSSVASVGDVVTITTCRASQGISISWLAHYQHOPGKAPKLLIYASASSLOGSVPSRF 62

QY      61 SSGSGYTDPSLTISLQPEDSATYYCOQANSFPTFGGKVEIK 105
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      63 SSGSGYTDPSLTISLQPEDPATYYCOQANSFPTFGGKVEIK 107
```

```
RESULT 13
US-11-254-182-27
; Sequence 27, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 27
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-254-182-27
```

```
Query Match      83.8%; Score 460; DB 7; Length 108;
Best Local Similarity 84.0%; Pred. No. 1.6e-35;
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
```

Oy	1	E L T O P S S S V A S V G R V I T T C R A S G I S M T A M Y H O K G K P K L I Y A S S I Q S V P S R F	60
	:	: : : : : :	:
Dd	3	Q M T Q S P S S L A S V G R V I T T C R A S G I S N Y L A M Y Q X R G K A P K L I Y A A S S J E S C V P S R F	62
Oy	61	S G S G V G D F S L T I S L O F E D S A T Y Y C Q Q A S P P Y F G G T K Y E I R	106
	:	: : : : : :	:
Dd	63	S G S G S G I D F I L T I S L O P E D F A T I Y C Q Q A I N S L P M T F G G T K Y E I R	108

```

Oy      61  SSSGGTDFSLTSLISLQCFEDSATYVCOOANSPPYFGQCTKVEIKR  106
Db      63  SSGSGTDFSLTSLISLQCFEDSATYVCOOANSPPYFGQCTKVEIKR  108

```

Search completed: August 30, 2006, 00:52:03  
Job time : 13.5273 secs

```

RESULT 14
US-11-219-121-23
: Sequence 23, Application US/111219121
: Publication No. US20060093601A1
GENERAL INFORMATION:
: APPLICANT: Fong, Sherman
: APPLICANT: Dennis Mark S.
: TITLE OF INVENTION: HUMANIZED ANTI-BEFA7 ANTAGONISTS AND USES THEREFOR
: FILE REFERENCE: P2159R1
: CURRENT APPLICATION NUMBER: US/11/219,121
: CURRENT FILING DATE: 2005-09-02
: PRIOR APPLICATION NUMBER: US 60/607,377
: PRIOR FILING DATE: 2004-09-03
: NUMBER OF SEQ ID NOS: 68
: SEQ ID NO 23
: LENGTH: 108
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: sequence is synthesized
US-11-219-121-23

```

```
Query Match      83.8%; Score 460; DB 7; Length 108;
Best Local Similarity -84.0%; Pred. No. 1.6e-35;
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0
```

```

QY      1 ELTQSSSVASVGDRTVITCRASQGISMTLAWQHQPCKAPKLLIYSASSLSQGVPSRF 600
        :::::::::::::::::::::::::::::
Db      3 QMTQSSSLASVGDRTVITCRASQGISNYLAWYQKPKCAPKLLIYAASSLSQGVPSRF 622

```

```
QY      61 SSGSYGDFSLTISLQFEDSATYYCQQA NSFPPTFGQGTKEIKR 106
        ||| :||| | | | | | | | | | | | | | | | | | | |
Db      63 SSGSGDFTLTIISSLDPEPATYYCQQA NSLPWTFGQTKEIKR 108
```

```

1  RESULT 15
2  US-11-106-762-19
3  : Sequence 19, Application US/11106762
4  : Publication No. US20060099662A1
5  : GENERAL INFORMATION:
6  : APPLICANT: CHUNTIARAPAI, ANN ET AL.
7  : TITLE OF INVENTION: ASSAY FOR ANTIBODIES
8  : FILE REFERENCE: F2075R1
9  : CURRENT APPLICATION NUMBER: US/11/106,762
10 : CURRENT FILING DATE: 2005-04-15
11 : PRIOR APPLICATION NUMBER: US 60/563,193
12 : PRIOR FILING DATE: 2004-04-16
13 : NUMBER OF SEQ ID NOS: 39
14 : SEQ ID NO 19
15 : LENGTH: 108
16 : TYPE: PRT
17 : ORGANISM: Artificial sequence
18 : FEATURE:
19 : OTHER INFORMATION: Sequence is synthesized
20 : US-11-106-762-19

```

Query Match	83.8%	Score 460;	DB 7;	Length 108;
Best Local Similarity	84.0%	Pred. No. 1.6e-35;		
Matches 89; Conservative	10;	Mismatches 7;	Indels 0;	Gaps 0

```

QY      1 ELTQSPSSVSASVGDRTVITTCRASQGISLWLTQHQPGRPKLLIYSASLSQGVPSRF 60
      :::::::::::::::::::::::::::::
Db      3 QMTQSPSSLSASVGDRTVITTCRASQGISNLTWLTQHQPGRPKLLIYAASLSLGVPSRF 62

```

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